

CC also be used to treat other conditions that involve angiogenesis, e.g.
 CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
 XX
 SQ Sequence 110 AA;

Query Match 100.0%; Score 575; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 5,4e-34;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTSPSSLSASVGDRTTITCSASQDISNLTMYQOKRGA PKVLIYFTSSLSHGVP 60
 DB 1 DIQLTSPSSLSASVGDRTTITCSASQDISNLTMYQOKRGA PKVLIYFTSSLSHGVP 60
 QY 61 RFGSGSGTDFLTITSSLOPEDPATYCCOYSTVPMFGGTVEIKRTV 110
 DB 61 RFGSGSGTDFLTITSSLOPEDPATYCCOYSTVPMFGGTVEIKRTV 110

RESULT 2

ID AAW70687 standard; peptide; 110 AA.

AC AAW70687;
 XX
 DT 27-JAN-1999 (first entry)

DE Anti-VEGF humanised antibody variable light domain of variant Y0317.

XX Light variable domain; murine; humanised antibody;

KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;

KW VEGF-induced angiogenesis; tumour; retinal disorder;

KW age-related macular degeneration; diabetic retinopathy;

KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

XX Synthetic.

OS Mus sp.

OS Homo sapiens.

XX MO9845331-A2.

XX 15-OCT-1998.

PD 03-APR-1998; 98WO-US006604.

PF 07-APR-1997; 97US-00833504.

PR 06-AUG-1997; 97US-00908469.

XX (GETH) GENENTECH INC.

PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

DR WPI; 1998-568337/48.

XX New humanised antibody with affinity for vascular endothelial growth

PT factor - for treatment of tumours, retinal disease and other angiogenic

PT states, also related nucleic acid, vectors and transformed cells.

XX Claim 27, Fig 10A, 100pp; English.

PS The present sequence represents a variable light domain of an affinity-

CC matured anti-vascular endothelial growth factor (anti-VEGF) antibody

CC variant. The sequence is used in the course of the invention to produce

CC the humanised anti-VEGF antibody of the invention. The humanised

CC antibodies are used to inhibit VEGF-induced angiogenesis, particularly

CC for treating or preventing tumours (of any type) and retinal disorders

CC (e.g. age-related macular degeneration or diabetic retinopathy). They can

CC also be used to treat other conditions that involve angiogenesis, e.g.

CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc

XX Sequence 110 AA;

SQ Query Match 100.0%; Score 575; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 5,4e-34;

Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTSPSSLSASVGDRTTITCSASQDISNLTMYQOKRGA PKVLIYFTSSLSHGVP 60
 DB 1 DIQLTSPSSLSASVGDRTTITCSASQDISNLTMYQOKRGA PKVLIYFTSSLSHGVP 60
 QY 61 RFGSGSGTDFLTITSSLOPEDPATYCCOYSTVPMFGGTVEIKRTV 110
 DB 61 RFGSGSGTDFLTITSSLOPEDPATYCCOYSTVPMFGGTVEIKRTV 110

RESULT 3

ID AAB13380 standard; protein; 110 AA.

AC AAB13380;
 XX
 DT 21-NOV-2000 (first entry)

DE Anti-VEGF antibody Y0317 light chain variable domain.

XX Y0317; vascular endothelial cell growth factor; VEGF; antibody;

KW antiinflammatory; cerebroprotective; cytostatic; antirheumatic;

KW antiarthritic; antiposrotic; antiarteriosclerotic; antidiabetic;

KW antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;

KW psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;

KW neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;

KW tissue transplantation; inflammation; oedema; trauma;

KW complementarity determining region; CDR.

XX Unidentified.

OS Key Location/Qualifiers

PH Region 24..33

FT Region /label= CDR-L1

FT Region 50..56

FT Region /label= CDR-L2

FT Region 69..97

FT Region /label= CDR-L3

XX MO200037502-A2.

XX 29-JUN-2000.

PD 09-DEC-1999; 99WO-US029475.

PF 22-DEC-1998; 98US-00218481.

XX (GETH) GENENTECH INC.

PI Van Bruggen N, Ferrara N;

DR WPI; 2000-442646/38.

XX Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,

PT diabetes and chronic inflammation in a mammal, comprises administering a

PT human vascular endothelial cell growth factor antagonist.

XX Disclosure; Fig 14A; 60pp; English.

XX The present sequence is the light chain variable region of the affinity

CC matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody

CC Y0317. Humanised F(ab)-12 and affinity matured anti-VEGF antibodies may

CC be used to treat conditions characterised by undesirable excessive

CC neovascularisation. Such conditions include tumours (especially solid

CC ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and

CC other retinopathies, retrolental fibroplasia, age-related macular

CC degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias

CC (including Grave's disease), corneal and other tissue transplantation,

CC and chronic inflammation. Oedemas associated with tumours, strokes and

CC head trauma, and ascites associated with malignancies, meigs's syndrome,

CC lung inflammation, nephrotic syndrome, pericardial effusion and pleural

CC effusion, may also be treated. Monoclonal antibodies are generated in

CC hybridoma cells and those with affinity for VEGF are identified by
CC immunoprecipitation or by an in vitro binding assay

XX Sequence 110 AA;

Query Match 100.0%; Score 575; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.4e-34;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSLASVGDRTVITTSASQDISNLYMTYQKRGKAPKVLIVFTSSLHSGVPS 60
DB 1 DIQLTQSPSLASVGDRTVITTSASQDISNLYMTYQKRGKAPKVLIVFTSSLHSGVPS 60

QY 61 RFGSGSGDFTLTISLQPEDPATYCCOYSTVPMTFGQGTVEIKRTV 110
DB 61 RFGSGSGDFTLTISLQPEDPATYCCOYSTVPMTFGQGTVEIKRTV 110

RESULT 4

ABP61256
ID ABP61256 standard; protein; 110 AA.

AC ABP61256;
DT 20-SEP-2002 (first entry)

DE Humanised anti-VEGF Y0317 antibody variable light domain.

XX Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
KM retinal disorder; intraocular neovascular disorder; Y0317; light chain;
XX variable domain.

OS Homo sapiens.
OS Mus sp.
OS Synthetic.

XX Location/Qualifiers

FT Domain 24..34
FT /label= CDR-L1
FT 50..56
FT /label= CDR-L2
FT 89..97
FT /label= CDR-L3

XX US2002032315-A1.

XX 14-MAR-2002.

XX 06-APR-1998; 98US-00056160.

XX 06-AUG-1997; 97US-0054856P.

XX (BACA/) BACA M.
PA (WELLS/) WELLS J A.
PA (PREST/) PRESTA L G.
PA (LOWM/) LOWMAN H B.
PA (CHEN/) CHEN Y M.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI, 2002-517920/55.

XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies
PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
PT mammal, particularly for treating tumor or retinal disorders.

XX Claim 27; Fig 10; 47pp; English.

XX The present invention relates to humanised anti-VEGF (vascular
CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),

CC particularly those having a tumour or a retinal disorder e.g. intraocular
CC neovascular disorders. The present sequence is an exemplary light chain
CC variable domain of the humanised anti-VEGF antibody of the invention

XX Sequence 110 AA;

Query Match 100.0%; Score 575; DB 5; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.4e-34;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSLASVGDRTVITTSASQDISNLYMTYQKRGKAPKVLIVFTSSLHSGVPS 60
DB 1 DIQLTQSPSLASVGDRTVITTSASQDISNLYMTYQKRGKAPKVLIVFTSSLHSGVPS 60

QY 61 RFGSGSGDFTLTISLQPEDPATYCCOYSTVPMTFGQGTVEIKRTV 110
DB 61 RFGSGSGDFTLTISLQPEDPATYCCOYSTVPMTFGQGTVEIKRTV 110

RESULT 5

ABP61246
ID ABP61246 standard; protein; 110 AA.

AC ABP61246;
DT 20-SEP-2002 (first entry)

DE Humanised anti-VEGF Y0101 antibody variable light domain.

XX Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
KM retinal disorder; intraocular neovascular disorder; Y0101; light chain;
XX variable domain.

OS Homo sapiens.
OS Mus sp.
OS Synthetic.

XX Location/Qualifiers

FT Domain 24..34
FT /label= CDR-L1
FT 50..57
FT /label= CDR-L2
FT 89..97
FT /label= CDR-L3

XX US2002032315-A1.

XX 14-MAR-2002.

XX 06-APR-1998; 98US-00056160.

XX 06-AUG-1997; 97US-0054856P.

XX (BACA/) BACA M.
PA (WELLS/) WELLS J A.
PA (PREST/) PRESTA L G.
PA (LOWM/) LOWMAN H B.
PA (CHEN/) CHEN Y M.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI, 2002-517920/55.

XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies
PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
PT mammal, particularly for treating tumor or retinal disorders.

XX Example 3; Fig 9; 47pp; English.

XX The present invention relates to humanised anti-VEGF (vascular
CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for

CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
 CC particularly those having a tumor or a retinal disorder e.g. intracocular
 CC neovascular disorders. The present sequence is an exemplary light chain
 CC variable domain of the humanised anti-VEGF antibody of the invention
 SQ
 Sequence 110 AA;

Query Match 100.0%; Score 575; DB 5; Length 110;
 Best Local Similarity 100.0%; Pred. No. 5, 4e-34;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCSASODISNTLNMVYQKRGKAPKYLIFTSLSHGVS 60
 DB 1 DIQLTQSPSSLSASVGDRTVITCSASODISNTLNMVYQKRGKAPKYLIFTSLSHGVS 60
 QY 61 RFGSGSGTDFLTITSSLOPEDPATYCCOYSTVPTWTFGGTKVEIKRTV 110
 DB 61 RFGSGSGTDFLTITSSLOPEDPATYCCOYSTVPTWTFGGTKVEIKRTV 110

RESULT 6
 ID ADC26154 standard; protein; 214 AA.
 AC ADC26154;

DT 18-DEC-2003 (first entry)
 DE Parent anti-VEGF Y0101 antibody wild-type light chain protein.

XX antibody variant; cytosstatic; cancer; parent; anti-VEGF;
 KM vascular endothelial growth factor; Y0101; light chain; wild-type.

OS Unidentified.
 PN WO2003068801-A2.
 PD 21-AUG-2003.

PF 11-FEB-2003; 2003WO-US004184.

PR 11-FEB-2002; 2002US-0355895P.
 PR 10-SEP-2002; 2002US-0409685P.

PA (GETH) GENENTECH INC.

PI Lowman HB, Marvin JS;

DR WPI: 2003-697521/66.

PT Making an antibody variant of a parent antibody specific to an antigen by
 PT identifying a target amino acid residue within the variable domain of the
 PT parent antibody and substituting the target residue with a different
 PT amino acid residue.

PS Example 1; SEQ ID NO 1; 81pp; English.

XX The invention relates to a novel method for making an antibody variant of
 CC a parent antibody specific to an antigen. This is achieved via
 CC identifying a target amino acid residue within the variable domain of the
 CC parent antibody and substituting the target residue with a different
 CC replacement amino acid residue such that the charge complementarity
 CC between the antibody and antigen is increased. The antibody variant of
 CC the invention demonstrates cytosstatic activity whilst the method may be
 CC useful for treating cancer. The current sequence is that of the parent
 CC anti-VEGF (vascular endothelial growth factor) Y0101 antibody wild-type
 CC light chain protein of the invention.

XX Sequence 214 AA;

Query Match 100.0%; Score 575; DB 7; Length 214;
 Best Local Similarity 100.0%; Pred. No. 9, 7e-34;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCSASODISNTLNMVYQKRGKAPKYLIFTSLSHGVS 60
 DB 1 DIQLTQSPSSLSASVGDRTVITCSASODISNTLNMVYQKRGKAPKYLIFTSLSHGVS 60

QY 61 RFGSGSGTDFLTITSSLOPEDPATYCCOYSTVPTWTFGGTKVEIKRTV 110
 DB 61 RFGSGSGTDFLTITSSLOPEDPATYCCOYSTVPTWTFGGTKVEIKRTV 110

RESULT 7
 ID ABB81107 standard; protein; 237 AA.
 AC ABB81107;

DT 05-NOV-2002 (first entry)
 DE Anti-VEGF light chain fragment.

XX Immunoglobulin; promoter; cytosstatic; antiinflammatory; immunomodulator;
 KM neuroprotective; CD11; tissue factor; vascular endothelial growth factor;
 KM VEGF.

OS Synthetic.

XX Key Location/Qualifiers
 FH 1..23
 FT Peptide /note="STII signal sequence TIR-1"

FT Protein /note="anti-VEGF light chain"

PN WO200261090-A2.
 PD 08-AUG-2002.

PF 13-DEC-2001; 2001WO-US048691.

PR 14-DEC-2000; 2000US-0256164P.

PA (GETH) GENENTECH INC.

PI Simmonds LC, Klimoweki L, Reilly DE, Vansura DG;

DR WPI: 2002-619253/66.

DR N-PSDB; ABB86646.

PT New polynucleotide comprising first and second promoter-cistron pairs,
 PT useful for diagnosing, treating or preventing diseases associated with
 PT abnormal expression and/or activity of antigens such as inflammatory
 PT disorders.

PS Disclosure; Fig 21A-C; 104pp; English.

XX The invention provides a polynucleotide, which encodes an immunoglobulin
 CC (Ig), comprising a first or second promoter-cistron pair consisting of a
 CC first or second promoter and cistron, respectively. The first cistron of
 CC the first promoter-cistron pair comprises a first translational
 CC initiation region (TIR-1) operably linked to a nucleic acid sequence
 CC encoding an Ig light chain and the second cistron of the second promoter-
 CC cistron pair comprises a second translational initiation region (TIR-2)
 CC operably linked to a nucleic acid sequence encoding an Ig heavy chain.
 CC Upon expression of the polynucleotide in a prokaryotic host cell, light
 CC and heavy chains are folded and assembled to form a biologically active
 CC Ig. The antibody of the invention is useful for diagnosing, treating or
 CC preventing diseases or conditions associated with abnormal expression and
 CC /or activity of one or more antigen molecules e.g. lymphoid malignancies,
 CC inflammatory, angiogenic, immunologic, neuronal, glial, astrocytal,
 CC hypothalamic or other glandular disorders. The present sequence
 CC represents the amino acid sequence of an anti-vascular endothelial growth
 CC factor (VEGF) light chain fragment of the cistron vector pVGA2AP11
 XX Sequence 237 AA;

Query Match 100.0%; Score 575; DB 5; Length 237;
 Best Local Similarity 100.0%; Pred. No. 1.1e-33;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTSPSSLSASVGRVITTCASODISNYLNMWQKPKAPKVLITYFTSSLSHGVPS 60
 DB 24 DIQLTSPSSLSASVGRVITTCASODISNYLNMWQKPKAPKVLITYFTSSLSHGVPS 83

QY 61 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 110
 DB 84 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 133

RESULT 8
 ABP51952
 ID ABP51952 standard; protein; 237 AA.
 XX
 AC ABP51952;
 XX
 DT 09-OCT-2002 (first entry)
 XX
 DE Plasmid pY0317 anti-VEGF Fab amino acid sequence SEQ ID NO:2 #1.
 XX
 KM Bacterial host; protease; degP; prc; spr; anti-VEGF antibody; antibody;
 KM humanised; Ap02 ligand; anti-CD18; anti-tissue factor; 2C4; anti-CD20;
 KM anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;
 KM anti-CD11a; Fab; Fab'2; Fab'2-leucine zipper fusion; anti-VEGF Fab.
 XX
 OS Mus sp.
 OS Escherichia coli.
 OS Synthetic.

Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= signal
 FT Protein 24..237
 FT /label= anti-VEGF_Fab

MO200248376-A2.
 XX
 PN 20-JUN-2002.
 XX
 PD 07-DEC-2001; 2001WO-US047581.
 XX
 PF 14-DEC-2000; 2000US-0256162P.
 XX
 PR (GETH) GENENTECH INC.
 PA
 PI Chen CY;
 XX
 PI WPI; 2002-583522/62.
 XX
 DR N-PSDB; ABQ73919.
 XX
 XX Novel Escherichia coli strain useful for producing polypeptide, deficient
 PT in degP and prc encoding protease, and harbouring mutant spr gene, product
 PT of gene suppresses growth phenotypes of strains harbouring prc mutants.
 XX
 PS Example 1; Fig 1A-C; 63pp; English.

CC The present invention describes an Escherichia coli strain (I) deficient
 CC in chromosomal degP and prc encoding protease and prc, respectively,
 CC and harbouring a mutant spr gene, the product of mutant spr gene
 CC suppresses growth phenotypes exhibited by strains harbouring prc mutants.
 CC (1) is useful for producing a polypeptide, by culturing (I) comprising
 CC nucleic acid encoding the polypeptide, which is heterologous to the
 CC strain, such that the nucleic acid is expressed, and recovering the
 CC heterologous polypeptide from the strain. The heterologous polypeptide is
 CC proteolytically sensitive. Culturing of (I) is performed in a fermentor
 CC under conditions of high- or low-cell density fermentation. The
 CC polypeptide is recovered from the periplasm or culture medium of the
 CC strain. The polypeptide is an antibody (humanised or full-length
 CC antibody) or Ap02 ligand. The antibody is an anti-CD18, anti-vascular

CC endothelial growth factor (VEGF), anti-tissue factor, 2C4, anti-Her-2,
 CC anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an
 CC antibody fragment having a light chain (kappa light chain). The antibody
 CC fragment is a Fab, Fab', Fab'2 or Fab'2-leucine zipper fusion, anti-CD18
 CC Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper
 CC fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-
 CC tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, or anti-
 CC CD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18
 CC Fab'2-leucine zipper fusion with a 6-lysine tag. The present sequence
 CC represents an anti-VEGF Fab amino acid sequence from the present
 CC invention
 XX
 XX Sequence 237 AA:

Query Match 100.0%; Score 575; DB 5; Length 237;
 Best Local Similarity 100.0%; Pred. No. 1.1e-33;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTSPSSLSASVGRVITTCASODISNYLNMWQKPKAPKVLITYFTSSLSHGVPS 60
 DB 24 DIQLTSPSSLSASVGRVITTCASODISNYLNMWQKPKAPKVLITYFTSSLSHGVPS 83

QY 61 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 110
 DB 84 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 133

RESULT 9
 ADO14128
 ID ADO14128 standard; protein; 237 AA.
 XX
 AC ADO14128;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Plasmid pXVG2AP11 expression cassette light chain protein SEQ ID NO:8.
 XX
 KM antibody; variant heavy chain hinge region; immunocombinator; cytostratic;
 KM immunosuppressive; immunotherapy; tumour; cancer; immune disorder;
 KM expression cassette; plasmid pXVG2AP11; anti-VEGF light chain.
 XX
 OS Synthetic.

MO2004042017-A2.
 XX
 PN 21-MAY-2004.
 XX
 PD 30-OCT-2003; 2003WO-US034610.
 XX
 PF 31-OCT-2002; 2002US-0422952P.
 XX
 PR (GETH) GENENTECH INC.
 PA
 PI Reilly D, Yansura DG;
 XX
 PI WPI; 2004-390607/36.
 XX
 DR N-PSDB; ADO14127.
 XX
 XX New antibody comprising a variant heavy chain hinge region incapable of
 PT inter-heavy chain disulfide linkage, useful for treating, preventing,
 PT diagnosing, delaying or preventing a disease, e.g. tumor, cancer or
 PT immune disorder.
 XX
 PS Example 1; SEQ ID NO 8; 124pp; English.

CC The present invention describes an antibody comprising a variant heavy
 CC chain hinge region incapable of inter-heavy chain disulfide linkage. Also
 CC described (1) an antibody lacking inter-heavy chain disulfide linkage;
 CC (2) an immunocombinator comprising the antibody conjugated with a
 CC heterologous moiety; (3) a composition comprising the antibody or
 CC immunocombinator, and carrier; (4) an article of manufacture comprising
 CC the composition in a container; (5) a polynucleotide encoding the
 CC antibody or immunocombinator, or a variant immunoglobulin heavy chain

```
CC immunconjugate, and carrier; (4) an article of manufacture comprising the
CC the composition in a container; (5) a polynucleotide encoding the
CC antibody or immunconjugate, or a variant immunoglobulin heavy chain
CC incapable of inter-heavy chain disulfide linkage; (6) a recombinant
CC vector for expressing the antibody or immunconjugate; (7) a host cell
CC comprising the recombinant vector; (8) expressing in a host cell an
CC antibody of interest in which at least one inter-heavy chain disulfide
CC linkage is eliminated, and recovering the antibody from the host cell;
CC (9) an aglycosylated antibody produced by the method; and (10) treating,
CC preventing, diagnosing, delaying or preventing a disease in a subject.
CC The antibody has cytostatic and immunosuppressive activities, and can be
CC used in immunotherapy. The antibody, immunconjugate and methods are
CC useful for treating, preventing, diagnosing, delaying or preventing a
CC disease, e.g. tumour, cancer or immune disorder. The present sequence
CC represents the anti-VEGF light chain from the expression cassette of
CC plasmid pVPCG11VERK, which is used in the exemplification of the present
CC invention.
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XX
XX Sequence 237 AA:
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```
SQ
SQ
SQ Query Match .100.0%; Score 575; DB 8; Length 237;
Beat Local Similarity 100.0%; Pred. No. 1.1e-33;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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OY 1 DIOGTQSPSSLSASVGRPVTTTCASODISNTLMWYQQKPKGAPKYLITYFTSSLHSGVPS 60
Db 24 DIOGTQSPSSLSASVGRPVITTCASODISNLTMLWYQQKPGAPKPLYIFTSSLHSGVPS 83
OY 61 RFSGSSTDPFTLTISSLQPEDPATYYCOQYSTVPWTGGCKVKELRTV 110
Db 84 RFSGSSTDPFTLTISSLQPEDPATYYCOQYSTVPWTGGCKVKELRTV 133
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RESULT 11
ADQ90703 standard; protein: 237 AA.
XX ADQ90703;
AC ADQ90703;
DC 21-OCT-2004 (first entry)
DT
XX Anti-VEGF antibody YO317 light chain protein SEQ ID NO:7.
DE
XX antibody; antigen binding fragment; cell culture; variable domain;
KW modified framework region; hypervariable region; cytostatic;
KW antiinflammatory; angiogenic; immunomodulatory; antibody therapy;
KW tumour; inflammatory disorder; angiogenic disorder;
KW immunological disorder; anti-VEGF antibody;
KW anti vascular endothelial cell growth factor antibody; light chain.
XX Homo sapiens.
OS Synthetic.
XX WO2004065417-A2.
XX
XX 05-AUG-2004.
XX PD
XX 23-JAN-2004; 2004WO-US001844.
XX PF
XX 23-JAN-2003; 2003US-0442484P.
XX PR
XX (GETH ) GENENTECH INC.
XX PA
XX Simmons L;
XX PI
XX WPI; 2004-562149/54.
DR N-PSDB; ADO90702.
XX
XX Producing an antibody or antigen binding fragment in high yield in a cell
PT culture, comprises expressing a variable domain with a modified framework
PT region in a host cell.
XX
XX Example 2; SEQ ID NO 7; 161pp; English.
XS
```

XX The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding
 CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents the light chain of an anti-VEGF (vascular endothelial
 CC cell growth factor) antibody, which is used in the exemplification of the
 CC present invention.

Sequence 237 AA;

Query Match 100.0%; Score 575; DB 8; Length 237;
 Best Local Similarity 100.0%; Pred. No. 1.1e-33;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQTGSPSSLSASVGDPRVTITCSASODISNYLNMVQOKPKAKPKVLIYFTSSLSHGVPS 60
 DB 24 DIQTGSPSSLSASVGDPRVTITCSASODISNYLNMVQOKPKAKPKVLIYFTSSLSHGVPS 83

QY 61 RFSGSGSGTDFTLTISLSLOPEDPATYVCOQYSTVPMTFGGGTKEIKRTV 110
 DB 84 RFSGSGSGTDFTLTISLSLOPEDPATYVCOQYSTVPMTFGGGTKEIKRTV 133

RESULT 12

ADQ90701
 XX ADQ90701 standard; protein; 237 AA.

ADQ90701;

XX 21-OCT-2004 (first entry)

DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:5.

XX antibody; antigen binding fragment; cell culture; variable domain;
 KW modified framework region; hypervariable region; cytostatic;
 KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; light chain.

OS Homo sapiens.
 OS Synthetic.

PN WO2004065417-A2.

XX 05-AUG-2004.

XX 23-JAN-2004; 2004WO-US001844.

XX 23-JAN-2003; 2003US-0442484P.

XX (GENTH) GENENTECH INC.

XX

PI Simmons L;

XX WPI; 2004-562149/54.
 DR N-PSDB; ADQ90700.

XX Producing an antibody or antigen binding fragment in high yield in a cell
 PT culture, comprises expressing a variable domain with a modified framework
 PT region in a host cell.

XX Example 2; SEQ ID NO 5; 161pp; English.

XX The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding
 CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents the light chain of an anti-VEGF (vascular endothelial
 CC cell growth factor) antibody, which is used in the exemplification of the
 CC present invention.

Sequence 237 AA;

Query Match 100.0%; Score 575; DB 8; Length 237;
 Best Local Similarity 100.0%; Pred. No. 1.1e-33;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQTGSPSSLSASVGDPRVTITCSASODISNYLNMVQOKPKAKPKVLIYFTSSLSHGVPS 60
 DB 24 DIQTGSPSSLSASVGDPRVTITCSASODISNYLNMVQOKPKAKPKVLIYFTSSLSHGVPS 83

QY 61 RFSGSGSGTDFTLTISLSLOPEDPATYVCOQYSTVPMTFGGGTKEIKRTV 110
 DB 84 RFSGSGSGTDFTLTISLSLOPEDPATYVCOQYSTVPMTFGGGTKEIKRTV 133

RESULT 13

ADQ90705
 XX ADQ90705 standard; protein; 237 AA.

ADQ90705;

XX 21-OCT-2004 (first entry)

DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:9.

XX antibody; antigen binding fragment; cell culture; variable domain;
 KW modified framework region; hypervariable region; cytostatic;
 KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; light chain.

OS Homo sapiens.
 OS Synthetic.

XX

```

PN WO2004065417-A2.
XX
XX 05-AUG-2004.
XX
XX 23-JAN-2004; 2004WO-US001844.
XX
XX 23-JAN-2003; 2003US-0442484P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Simmone L;
XX
XX WPI; 2004-562149/54.
XX
XX N-PSDB; ADO90704.
XX
XX Producing an antibody or antigen binding fragment in high yield in a cell
XX culture, comprises expressing a variable domain with a modified framework
XX region in a host cell.
XX
XX Example 2; SEQ ID NO 9; 161bp; English.
XX
XX The present invention describes a method for producing an antibody or
XX antigen binding fragment in high yield in a cell culture. The method
XX comprises expressing a variable domain of the antibody or antigen binding
XX fragment comprising a modified framework region (FR) in a host cell, and
XX recovering the antibody or antigen binding fragment variable domain
XX comprising the modified framework from the host cell. The modified FR in
XX the method described above has a substitution of at least one amino acid
XX position with a different amino acid, where the different amino acid is
XX the amino acid found at the corresponding FR position of a human subgroup
XX (HVR1) and/or HVR2 amino acid sequence that has a hypervariable region 1
XX with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
XX The antibody or antigen binding fragment variable domain comprises the
XX modified FR that has improved yield in cell culture compared to an
XX unmodified antibody or antigen-binding fragment. The antibody and antigen
XX binding fragment have cytostatic, antiinflammatory, antiangiogenic and
XX immunomodulatory activities, and can be used in antibody therapy. The
XX methods and compositions of the present invention are useful for
XX producing antibodies or antigen binding fragments in cell culture, in
XX particular for improving the yield of recombinant antibodies or antigen
XX binding fragments in cell culture. The antibodies of the invention can be
XX used to diagnose, treat, inhibit or prevent e.g. tumours and
XX inflammatory, angiogenic and immunological disorders. The present
XX sequence represents the light chain of an anti-VEGF (vascular endothelial
XX cell growth factor) antibody, which is used in the exemplification of the
XX present invention.
XX
XX Sequence 237 AA;
XX
XX Query Match 100.0%; Score 575; DB 8; Length 237;
XX Best Local Similarity 100.0%; Pred. No. 1,1e-33;
XX Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 DIQLTQSPSSLSASVGVDRVTITCSASODISNYLWYQKPKAKPKVLIYFTSLHSGVPS 60
DB 24 DIQLTQSPSSLSASVGVDRVTITCSASODISNYLWYQKPKAKPKVLIYFTSLHSGVPS 83
OY 61 RFGSGSGGTDFLTITSLQPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 110
DB 84 RFGSGSGGTDFLTITSLQPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 133
XX
XX RESULT 14
XX ADO90709 standard; protein; 237 AA.
XX
XX ADO90709;
XX
XX 21-OCT-2004 (first entry)
XX
XX Anti-VEGF antibody VNERK light chain protein SEQ ID NO:13.
XX

```

```

KW antibody; antigen binding fragment; cell culture; variable domain;
KW modified framework region; hypervariable region; cytostatic;
KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
KW tumour; inflammatory disorder; angiogenic disorder;
KW immunological disorder; anti-VEGF antibody;
KW anti vascular endothelial cell growth factor antibody; light chain.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO2004065417-A2.
XX
XX 05-AUG-2004.
XX
XX 23-JAN-2004; 2004WO-US001844.
XX
XX 23-JAN-2003; 2003US-0442484P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Simmone L;
XX
XX WPI; 2004-562149/54.
XX
XX N-PSDB; ADO90708.
XX
XX Producing an antibody or antigen binding fragment in high yield in a cell
XX culture, comprises expressing a variable domain with a modified framework
XX region in a host cell.
XX
XX Example 2; SEQ ID NO 13; 161bp; English.
XX
XX The present invention describes a method for producing an antibody or
XX antigen binding fragment in high yield in a cell culture. The method
XX comprises expressing a variable domain of the antibody or antigen binding
XX fragment comprising a modified framework region (FR) in a host cell, and
XX recovering the antibody or antigen binding fragment variable domain
XX comprising the modified framework from the host cell. The modified FR in
XX the method described above has a substitution of at least one amino acid
XX position with a different amino acid, where the different amino acid is
XX the amino acid found at the corresponding FR position of a human subgroup
XX (HVR1) and/or HVR2 amino acid sequence that has a hypervariable region 1
XX with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
XX The antibody or antigen binding fragment variable domain comprises the
XX modified FR that has improved yield in cell culture compared to an
XX unmodified antibody or antigen-binding fragment. The antibody and antigen
XX binding fragment have cytostatic, antiinflammatory, antiangiogenic and
XX immunomodulatory activities, and can be used in antibody therapy. The
XX methods and compositions of the present invention are useful for
XX producing antibodies or antigen binding fragments in cell culture, in
XX particular for improving the yield of recombinant antibodies or antigen
XX binding fragments in cell culture. The antibodies of the invention can be
XX used to diagnose, treat, inhibit or prevent e.g. tumours and
XX inflammatory, angiogenic and immunological disorders. The present
XX sequence represents the light chain of an anti-VEGF (vascular endothelial
XX cell growth factor) antibody, which is used in the exemplification of the
XX present invention.
XX
XX Sequence 237 AA;
XX
XX Query Match 100.0%; Score 575; DB 8; Length 237;
XX Best Local Similarity 100.0%; Pred. No. 1,1e-33;
XX Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 DIQLTQSPSSLSASVGVDRVTITCSASODISNYLWYQKPKAKPKVLIYFTSLHSGVPS 60
DB 24 DIQLTQSPSSLSASVGVDRVTITCSASODISNYLWYQKPKAKPKVLIYFTSLHSGVPS 83
OY 61 RFGSGSGGTDFLTITSLQPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 110
DB 84 RFGSGSGGTDFLTITSLQPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 133
XX

```

RESULT 15

ADQ90723

ID ADQ90723 standard; protein; 237 AA.

AC ADQ90723;

DT 21-OCT-2004 (first entry)

DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:27.

KW antibody; antigen binding fragment; cell culture; variable domain;

KW modified framework region; hypervariable region; cytosolic;

KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;

KW tumour; inflammatory disorder; angiogenic disorder;

KW immunological disorder; anti-VEGF antibody;

KW anti vascular endothelial cell growth factor antibody; light chain.

XX Homo sapiens.

XX Synthetic.

XX WO2004065417-A2.

XX 05-AUG-2004.

XX 23-JAN-2004; 2004WO-US001844.

XX 23-JAN-2003; 2003US-0442484P.

XX (GETH) GENENTECH INC.

XX Simmons L;

XX WPI; 2004-562149/54.

XX N-PSDB; ADQ90722.

XX Producing an antibody or antigen binding fragment in high yield in a cell

XX culture, comprises expressing a variable domain with a modified framework

XX region in a host cell.

XX Example 7; SEQ ID NO 27; 161pp; English.

XX The present invention describes a method for producing an antibody or

XX antigen binding fragment in high yield in a cell culture. The method

XX comprises expressing a variable domain of the antibody or antigen binding

XX fragment comprising a modified framework region (FR) in a host cell, and

XX recovering the antibody or antigen binding fragment variable domain

XX comprising the modified framework from the host cell. The modified FR in

XX the method described above has a substitution of at least one amino acid

XX position with a different amino acid, where the different amino acid is

XX the amino acid found at the corresponding FR position of a human subgroup

XX (HVR1) and/or HVR2 amino acid sequence that has a hypervariable region 1

XX with a corresponding HVR1 and/or HVR2 sequence of the variable domain.

XX The antibody or antigen binding fragment variable domain comprises the

XX modified FR that has improved yield in cell culture compared to an

XX unmodified antibody or antigen-binding fragment. The antibody and antigen

XX binding fragment have cytostatic, antiinflammatory, antiangiogenic and

XX immunomodulatory activities, and can be used in antibody therapy. The

XX methods and compositions of the present invention are useful for

XX producing antibodies or antigen binding fragments in cell culture, in

XX particular for improving the yield of recombinant antibodies or antigen

XX binding fragments in cell culture. The antibodies of the invention can be

XX used to diagnose, treat, inhibit or prevent e.g. tumours and

XX inflammatory, angiogenic and immunological disorders. The present

XX sequence represents the light chain of an anti-VEGF (vascular endothelial

XX cell growth factor) antibody, which is used in the exemplification of the

XX present invention.

XX Sequence 237 AA;

SQ

QY 1 DIQLTQSPSSLSASVGDPRVTITCSASODISNYLNMVQOKRGKAPKYLIVETSSLHSGVPS 60

DB 24 DIQLTQSPSSLSASVGDPRVTITCSASODISNYLNMVQOKRGKAPKYLIVETSSLHSGVPS 83

QY 61 RPSGSGSGTDFLTITSSLPEDPATYCCQYSTVPTWTFGQGTKEIKRTV 110

DB 84 RPSGSGSGTDFLTITSSLPEDPATYCCQYSTVPTWTFGQGTKEIKRTV 133

Search completed: March 14, 2005, 20:39:16

Job time : 88.0482 secs

Query Match 100.0%; Score 575; DB 8; Length 237;

Best Local Similarity 100.0%; Pred. No. 1,1e-33;

Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2005, 20:30:13 ; Search time 22.6754 Seconds
(without alignments)
362.127 Million cell updates/sec

Title: US-09-723-752B-115
Perfect score: 575
Sequence: 1 DIQQTSPSSLSASVGRVT.....YSTVPMFGQTKYIKRTV 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573	99.7	110	US-09-440-781-94	Sequence 94, Appl
2	569	99.0	491	US-10-011-125A-2	Sequence 2, Appl
3	556	96.7	110	US-09-440-781-95	Sequence 95, Appl
4	522	90.8	214	US-07-934-373C-40	Sequence 40, Appl
5	522	90.8	214	US-08-788-800-11	Sequence 11, Appl
6	522	90.8	214	US-08-437-642B-40	Sequence 40, Appl
7	522	90.8	214	US-09-097-1309-2	Sequence 2, Appl
8	522	90.8	214	US-09-097-1309-2	Sequence 2, Appl
9	522	90.8	214	US-09-460-587-2	Sequence 2, Appl
10	522	90.8	214	US-09-940-166A-2	Sequence 2, Appl
11	522	90.8	214	PCT-US93-07832-40	Sequence 40, Appl
12	522	90.8	233	US-07-934-373C-25	Sequence 25, Appl
13	522	90.8	233	US-08-437-642B-25	Sequence 25, Appl
14	522	90.8	233	US-08-146-206C-25	Sequence 25, Appl
15	522	90.8	233	US-09-705-686-25	Sequence 25, Appl
16	522	90.8	233	US-09-705-392A-25	Sequence 25, Appl
17	522	90.8	233	US-09-705-398-25	Sequence 25, Appl
18	522	90.8	233	PCT-US93-07832-25	Sequence 25, Appl
19	522	90.8	237	US-09-097-1309-6	Sequence 6, Appl
20	522	90.8	237	US-09-097-1309-6	Sequence 6, Appl
21	522	90.8	237	US-09-423-712B-2	Sequence 2, Appl
22	522	90.8	237	US-09-607-756-2	Sequence 2, Appl
23	522	90.8	237	US-09-460-587-6	Sequence 6, Appl
24	522	90.8	237	US-09-940-166A-6	Sequence 6, Appl
25	519	90.3	214	US-08-458-516-12	Sequence 12, Appl
26	518	90.1	109	US-07-934-373C-47	Sequence 47, Appl
27	518	90.1	109	US-08-437-642B-47	Sequence 47, Appl

28	514	89.4	214	2	US-07-934-373C-39	Sequence 39, Appl
29	514	89.4	214	3	US-08-437-642B-39	Sequence 39, Appl
30	514	89.4	214	5	PCT-US93-07832-39	Sequence 39, Appl
31	511	88.9	107	2	US-07-934-373C-17	Sequence 17, Appl
32	511	88.9	107	3	US-08-437-642B-17	Sequence 17, Appl
33	511	88.9	107	4	US-08-146-206C-17	Sequence 17, Appl
34	511	88.9	107	4	US-09-705-686-17	Sequence 17, Appl
35	511	88.9	107	4	US-09-705-392A-17	Sequence 17, Appl
36	511	88.9	107	4	US-09-705-398-17	Sequence 17, Appl
37	511	88.9	107	5	PCT-US93-07832-17	Sequence 17, Appl
38	511	88.9	108	3	US-08-974-899-3	Sequence 3, Appl
39	511	88.9	108	4	US-09-795-798-3	Sequence 3, Appl
40	511	88.9	127	3	US-08-649-100-33	Sequence 33, Appl
41	507	88.2	109	2	US-07-934-373C-3	Sequence 3, Appl
42	507	88.2	109	3	US-08-437-642B-3	Sequence 3, Appl
43	507	88.2	109	4	US-08-146-206C-3	Sequence 3, Appl
44	507	88.2	109	4	US-09-705-686-3	Sequence 3, Appl
45	507	88.2	109	4	US-09-705-392A-3	Sequence 3, Appl

ALIGNMENTS

```

RESULT 1
US-09-440-781-94
Sequence 94, Application US/09440781
Patent No. 6632826
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yeet Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 94
LENGTH: 110
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-110
OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-94

Query Match          99.7%; Score 573; DB 4; Length 110;
Best Local Similarity 99.1%; Pred. No. 8.6e-47;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy      1 DIQQTSPSSLSASVGRVTITCSASODISNLTWYQKPKAKRVLITFTSLHSGVPS 60
      |||:|||||
Db      1 DIQQTSPSSLSASVGRVTITCSASODISNLTWYQKPKAKRVLITFTSLHSGVPS 60
      |||:|||||

Cy      61 RFSSSGGTFTLTITSSLOPEDFATYVCOQSTVPMFGQTKYIKRTV 110
      |||:|||||
Db      61 RFSSSGGTFTLTITSSLOPEDFATYVCOQSTVPMFGQTKYIKRTV 110
      |||:|||||

RESULT 2
US-10-011-125A-2
Sequence 2, Application US/1001125A
Patent No. 6828121
GENERAL INFORMATION:
APPLICANT: Chen, Christina Yu-Ching
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1804R1
CURRENT APPLICATION NUMBER: US/10/011,125A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 2
LENGTH: 491
TYPE: PRT

```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
US-10-011-125A-2

Query Match          99.0%; Score 569; DB 4; Length 491;
Best Local Similarity 98.2%; Pred. No. 1.1e-45;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTVITCSASQDISNTLNTWYQKPKAPKVLITYFTSSLHSGVPS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 24 DIQLTQSPSSLSASVGDRTVITCSASQDISNTLNTWYQKPKAPKVLITYFTSSLHSGVPS 83
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 RPSGSGSGTDFLTITSSLPEDPATYCCQYSTVPMTFGQGTKEIKRTV 110
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 84 RPSGSGSGTDFLTITSSLPEDPATYCCQYSTVPMTFGQGTKEIKRTV 133
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
US-09-440-781-95
; Sequence 95, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 95
; LENGTH: 110
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-110
; OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-95

Query Match          96.7%; Score 556; DB 4; Length 110;
Best Local Similarity 95.5%; Pred. No. 3.4e-45;
Matches 105; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQLTQSPSSLSASVGDRTVITCRANEQSLNTLNTWYQKPKAPKVLITYFTSSLHSGVPS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 RPSGSGSGTDFLTITSSLPEDPATYCCQYSTVPMTFGQGTKEIKRTV 110
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RPSGSGSGTDFLTITSSLPEDPATYCCQYSTVPMTFGQGTKEIKRTV 110
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
US-07-934-373C-40
; Sequence 40, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```

; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-40

Query Match          90.8%; Score 522; DB 2; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTVITCSASQDISNTLNTWYQKPKAPKVLITYFTSSLHSGVPS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQDISNTLNTWYQKPKAPKVLITYFTSSLHSGVPS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 RPSGSGSGTDFLTITSSLPEDPATYCCQYSTVPMTFGQGTKEIKRTV 110
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RPSGSGSGTDFLTITSSLPEDPATYCCQYSTVPMTFGQGTKEIKRTV 110
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
US-08-788-800-11
; Sequence 11, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0887x1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 11:
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SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-788-800-11

Query Match 90.8%; Score 522; DB 2; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCASQDISNYLNMWYQKPKAPKVLITYFTSLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQDINNINLMWYQKPKAPKVLITYFTSLHSGVPS 60
QY 61 RFGSGSGGTDTYTLTISLSLOPEDFATYYCQOYSTVPMTFGGGTKEIKRTV 110
DB 61 RFGSGSGGTDTYTLTISLSLOPEDFATYYCQOQGNLTPFTGGGTKEIKRTV 110

RESULT 6

US-08-437-642B-40
Sequence 40, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-40

Query Match 90.8%; Score 522; DB 3; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCASQDISNYLNMWYQKPKAPKVLITYFTSLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQDINNINLMWYQKPKAPKVLITYFTSLHSGVPS 60
QY 61 RFGSGSGGTDTYTLTISLSLOPEDFATYYCQOYSTVPMTFGGGTKEIKRTV 110
DB 61 RFGSGSGGTDTYTLTISLSLOPEDFATYYCQOQGNLTPFTGGGTKEIKRTV 110

RESULT 7

US-09-097-309-2
Sequence 2, Application US/09097309
Patent No. 6121428
GENERAL INFORMATION:
APPLICANT: Blank, Gregory S.
APPLICANT: Natindray, Daljit S.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,309
FILING DATE: 12-Jun-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050951
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELEPHONE: 650/225-7467
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-097-309-2

Query Match 90.8%; Score 522; DB 3; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCASQDISNYLNMWYQKPKAPKVLITYFTSLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQDINNINLMWYQKPKAPKVLITYFTSLHSGVPS 60
QY 61 RFGSGSGGTDTYTLTISLSLOPEDFATYYCQOYSTVPMTFGGGTKEIKRTV 110
DB 61 RFGSGSGGTDTYTLTISLSLOPEDFATYYCQOQGNLTPFTGGGTKEIKRTV 110

RESULT 8

US-09-097-171A-2
Sequence 2, Application US/09097171A
Patent No. 6171586
GENERAL INFORMATION:
APPLICANT: Lam, Xanthe M.
APPLICANT: Osweil, James Q.

APPLICANT: Ongpattanakul, Boonert
APPLICANT: Shantokh, Zaira
APPLICANT: Wang, Sharon X.
APPLICANT: Weisburg, Robert P.
APPLICANT: Wong, Rita L.
TITLE OF INVENTION: Antibody Formulation
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,171A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/874897
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1089R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-097-171A-2
Query Match 90.8%; Score 522; DB 3; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTVITCSASQDISNINMYQKPGKAPKLIYFTSLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNINMYQKPGKAPKLIYFTSLHSGVPS 60
QY 61 RPSGSGSDTFTLTISLQPEDPATYCCQYSTVPTFGQTKVEIKRTV 110
DB 61 RPSGSGSDTFTLTISLQPEDPATYCCQGNLTLPPTFGQTKVEIKRTV 110
RESULT 9
US-09-460-587-2
Sequence 2, Application US/09460587
Patent No. 6322997
GENERAL INFORMATION:
APPLICANT: Blank, Gregory S.
APPLICANT: Narindray, Daljit S.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460,587
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/097,309
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-460-587-2
Query Match 90.8%; Score 522; DB 3; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTVITCSASQDISNINMYQKPGKAPKLIYFTSLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNINMYQKPGKAPKLIYFTSLHSGVPS 60
QY 61 RPSGSGSDTFTLTISLQPEDPATYCCQYSTVPTFGQTKVEIKRTV 110
DB 61 RPSGSGSDTFTLTISLQPEDPATYCCQGNLTLPPTFGQTKVEIKRTV 110
RESULT 10
US-09-940-166A-2
Sequence 2, Application US/09940166A
Patent No. 6716598
GENERAL INFORMATION:
APPLICANT: Blank, Gregory S.
APPLICANT: Narindray, Daljit S.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/940,166A
FILING DATE: 27-Aug-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/097,309
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-940-166A-2

Query Match 90.8%; Score 522, DB 4; Length 214;
Best Local Similarity 90.0%; Pred. No. 1,1e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQLTGSSSLASVGVGRVITTCRASQDINSYLNWYQKPKAPKVLITYTSLHSGVPS 60
DB 1 DIQLTGSSSLASVGVGRVITTCRASQDINSYLNWYQKPKAPKVLITYTSLHSGVPS 60
QY 61 RFGSGSGTDFTLTISLQPEDPATYTCQOYSTVPMTFGGTKVEIKRTV 110
DB 61 RFGSGSGTDFTLTISLQPEDPATYTCQOYSTVPMTFGGTKVEIKRTV 110

RESULT 11
PCT-US93-07832-40
Sequence 40, Application PC/TUS9307832
GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Pointe San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/115272

FILING DATE: 14-JUN-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/05126

FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/934373

FILING DATE: 21-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME:

REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER: 709P2PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE:

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 214 amino acids

TYPE: amino acid

TOPOLOGY: Linear

PCT-US93-07832-40

Query Match 90.8%; Score 522, DB 5; Length 214;
Best Local Similarity 90.0%; Pred. No. 1,1e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQLTGSSSLASVGVGRVITTCRASQDINSYLNWYQKPKAPKVLITYTSLHSGVPS 60
DB 1 DIQLTGSSSLASVGVGRVITTCRASQDINSYLNWYQKPKAPKVLITYTSLHSGVPS 60

DB 1 DIQLTGSSSLASVGVGRVITTCRASQDINSYLNWYQKPKAPKVLITYTSLHSGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDPATYTCQOYSTVPMTFGGTKVEIKRTV 110
DB 61 RFGSGSGTDFTLTISLQPEDPATYTCQOYSTVPMTFGGTKVEIKRTV 110

RESULT 12
US-07-934-373C-25
Sequence 25, Application US/07934373C
Patent No. 5821337

GENERAL INFORMATION:

APPLICANT: Paul J. Carter

APPLICANT: Leonard G. Presta

TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPacIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/934,373C

FILING DATE: 21-Aug-1992

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/05126

FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/715272

FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P0709P2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 233 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-07-934-373C-25

Query Match 90.8%; Score 522, DB 2; Length 233;
Best Local Similarity 90.0%; Pred. No. 1,1e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQLTGSSSLASVGVGRVITTCRASQDINSYLNWYQKPKAPKVLITYTSLHSGVPS 60
DB 20 DIQLTGSSSLASVGVGRVITTCRASQDINSYLNWYQKPKAPKVLITYTSLHSGVPS 79

QY 61 RFGSGSGTDFTLTISLQPEDPATYTCQOYSTVPMTFGGTKVEIKRTV 110
DB 80 RFGSGSGTDFTLTISLQPEDPATYTCQOYSTVPMTFGGTKVEIKRTV 129

RESULT 13
US-08-437-642B-25
Sequence 25, Application US/08437642B
Patent No. 6054297

GENERAL INFORMATION:

APPLICANT: Paul J. Carter

APPLICANT: Leonard G. Presta

TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P07092C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-25

Query Match 90.8%; Score 522; DB 3; Length 233;
Best Local Similarity 90.0%; Pred. No. 1.3e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQLQSPSSLSASVGDVVTTCASODISNYLNWYQOKPKAPKVLIVFTSSLSHGVPS 60
DB 20 DIQMTQSPSSLSASVGDVVTTCASODINNYLNWYQOKPKAPKVLIVFTSSLSHGVPS 79

QY 61 RFSGSGGTDTLTITSSLPEDPATYCCQYSTVPMWTFGQTKVEIKRTV 110
DB 80 RFSGSGGTDTLTITSSLPEDPATYCCQGNLTLPFTFGQTKVEIKRTV 129

RESULT 14
US-08-146-206C-25
Sequence 25, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presca, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-25

Query Match 90.8%; Score 522; DB 4; Length 233;
Best Local Similarity 90.0%; Pred. No. 1.3e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQLQSPSSLSASVGDVVTTCASODISNYLNWYQOKPKAPKVLIVFTSSLSHGVPS 60
DB 20 DIQMTQSPSSLSASVGDVVTTCASODINNYLNWYQOKPKAPKVLIVFTSSLSHGVPS 79

QY 61 RFSGSGGTDTLTITSSLPEDPATYCCQYSTVPMWTFGQTKVEIKRTV 110
DB 80 RFSGSGGTDTLTITSSLPEDPATYCCQGNLTLPFTFGQTKVEIKRTV 129

RESULT 15
US-09-705-686-25
Sequence 25, Application US/09705686
Patent No. 6639055
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presca, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-705-686-25

Query Match 90.8%; Score 522; DB 4; Length 233;
Best Local Similarity 90.0%; Pred. No. 1.3e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY	1	DIQLTGSPSSISASVGRVTITCSASODISNYLWYQKPGKAPKVLITYFTSLHSGVPS	60
Db	20	DIQWTGSPSSISASVGRVTITCRASQDINNYLWYQKPGKAPKVLITYFTSLHSGVPS	79
QY	61	RFGSGSGCTDFTLTISSIQPEDFATYYCOQSTVPMTFGCTKVEIKRTV	110
Db	80	RFGSGSGCTDFTLTISSIQPEDFATYYCOQGNLPLPTFGCTKVEIKRTV	129

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Job time : 22.6754 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 14, 2005, 20:22:02 ; Search time 41.0088 seconds

(without alignments)
884.760 Million cell updates/sec

Title: US-09-723-752B-115

Perfect score: 575
Sequence: 1 DIQLTSPSSLSASVGDRTV.....YSTVPTFGGCTKVEIKRTV 110Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
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- 6: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep:*
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- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
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- 20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	575	100.0	110	9	US-09-056-160B-117
3	575	100.0	110	14	US-10-234-671-105
4	575	100.0	110	14	US-10-234-671-115
5	575	100.0	213	16	US-10-379-392-135
6	575	100.0	213	16	US-10-379-392-137
7	575	100.0	213	16	US-10-379-392-139
8	575	100.0	214	16	US-10-364-953-1
9	575	100.0	237	14	US-10-020-786-10
10	575	100.0	237	17	US-10-697-995-8
11	575	100.0	237	17	US-10-697-995-11
12	573	99.7	110	14	US-10-234-671-8
13	573	99.7	110	15	US-10-624-153-94

14	572	99.5	110	9	US-09-056-160B-105	Sequence 105, App
15	572	99.5	110	14	US-10-234-671-103	Sequence 103, App
16	571	99.3	213	16	US-10-379-392-155	Sequence 155, App
17	570	99.1	213	16	US-10-379-392-153	Sequence 153, App
18	569	99.0	110	9	US-09-056-160B-103	Sequence 103, App
19	569	99.0	110	14	US-10-234-671-101	Sequence 101, App
20	569	99.0	237	9	US-09-056-160B-100	Sequence 100, App
21	569	99.0	237	14	US-10-234-671-100	Sequence 100, App
22	569	99.0	491	13	US-10-011-125-2	Sequence 2, App
23	567	98.6	213	13	US-10-379-392-157	Sequence 157, App
24	566	98.4	108	13	US-10-153-159-4	Sequence 4, App1
25	566	98.4	108	15	US-10-153-176-4	Sequence 4, App1
26	566	98.4	108	15	US-10-443-134A-4	Sequence 4, App1
27	564	98.1	108	9	US-09-056-160B-8	Sequence 8, App1
28	564	98.1	108	13	US-10-153-159-2	Sequence 2, App1
29	564	98.1	108	13	US-10-153-159-16	Sequence 16, App1
30	564	98.1	108	14	US-10-153-176-2	Sequence 2, App1
31	564	98.1	108	14	US-10-153-176-16	Sequence 16, App1
32	564	98.1	108	15	US-10-443-134A-2	Sequence 2, App1
33	564	98.1	108	15	US-10-443-134A-16	Sequence 16, App1
34	564	98.1	108	15	US-10-443-134A-127	Sequence 127, App
35	564	98.1	108	17	US-10-877-532-7	Sequence 7, App1
36	561	97.6	108	9	US-09-056-160B-126	Sequence 126, App
37	561	97.6	108	14	US-10-234-671-124	Sequence 124, App
38	559	97.2	107	16	US-10-723-434-1	Sequence 1, App1
39	558	97.0	214	15	US-10-364-953-4	Sequence 4, App1
40	557	96.9	214	15	US-10-364-953-3	Sequence 3, App1
41	556	96.7	107	9	US-09-056-160B-13	Sequence 13, App1
42	556	96.7	107	14	US-10-234-671-13	Sequence 13, App1
43	556	96.7	110	9	US-09-056-160B-109	Sequence 109, App
44	556	96.7	110	9	US-09-056-160B-111	Sequence 111, App
45	556	96.7	110	9	US-09-056-160B-113	Sequence 113, App

ALIGNMENTS

RESULT 1
US-09-056-160B-107
Sequence 107, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Beca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haeak, Janet B.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:

Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Weile, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-Apr-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-Apr-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-10-234-671-115
Query Match 100.0%; Score 575; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.8e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQLTQSPSSLSASVGRVTITCSASODISNYLNMWYQKPKAKPKVLIYFTSSLHSGVPS 60
Db 1 DIQLTQSPSSLSASVGRVTITCSASODISNYLNMWYQKPKAKPKVLIYFTSSLHSGVPS 60
Qy 61 RPSGSGGTDFTLTITSSLPEDPATYCCQYSTVPMWFGGTKEIKRTV 110
Db 61 RPSGSGGTDFTLTITSSLPEDPATYCCQYSTVPMWFGGTKEIKRTV 110
Db 61 RPSGSGGTDFTLTITSSLPEDPATYCCQYSTVPMWFGGTKEIKRTV 110
RESULT 5
US-10-379-392-135
Sequence 135, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
Deesjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahlvat, Baasil I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 135
LENGTH: 213
TYPE: PRT
ORGANISM: Unknown
FEATURES:
OTHER INFORMATION: Humanized
US-10-379-392-135
Query Match 100.0%; Score 575; DB 16; Length 213;
Best Local Similarity 100.0%; Pred. No. 3.3e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQLTQSPSSLSASVGRVTITCSASODISNYLNMWYQKPKAKPKVLIYFTSSLHSGVPS 60
Db 1 DIQLTQSPSSLSASVGRVTITCSASODISNYLNMWYQKPKAKPKVLIYFTSSLHSGVPS 60
Qy 61 RPSGSGGTDFTLTITSSLPEDPATYCCQYSTVPMWFGGTKEIKRTV 110
Db 61 RPSGSGGTDFTLTITSSLPEDPATYCCQYSTVPMWFGGTKEIKRTV 110
Db 61 RPSGSGGTDFTLTITSSLPEDPATYCCQYSTVPMWFGGTKEIKRTV 110
RESULT 7
US-10-379-392-139
Sequence 139, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
Deesjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahlvat, Baasil I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 137
LENGTH: 213
TYPE: PRT
ORGANISM: Artificial sequence
FEATURES:
OTHER INFORMATION: Synthetic
US-10-379-392-137
Query Match 100.0%; Score 575; DB 16; Length 213;
Best Local Similarity 100.0%; Pred. No. 3.3e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQLTQSPSSLSASVGRVTITCSASODISNYLNMWYQKPKAKPKVLIYFTSSLHSGVPS 60
Db 1 DIQLTQSPSSLSASVGRVTITCSASODISNYLNMWYQKPKAKPKVLIYFTSSLHSGVPS 60
Qy 61 RPSGSGGTDFTLTITSSLPEDPATYCCQYSTVPMWFGGTKEIKRTV 110
Db 61 RPSGSGGTDFTLTITSSLPEDPATYCCQYSTVPMWFGGTKEIKRTV 110
Db 61 RPSGSGGTDFTLTITSSLPEDPATYCCQYSTVPMWFGGTKEIKRTV 110

```

; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basail I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: Patentin version 3.2
; SEQ ID NO: 139
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (116)..(116)
; OTHER INFORMATION: Xaa at position 116 can be Phe or Tyr
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (133)..(133)
; OTHER INFORMATION: Xaa at position 133 can be Ile, Met or Val
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (135)..(135)
; OTHER INFORMATION: Xaa at position 135 can be Leu, Ile or Met
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (176)..(176)
; OTHER INFORMATION: Xaa at position 176 can be Met, Val, Ala or Ser
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (178)..(178)
; OTHER INFORMATION: Xaa at position 178 can be Met, Thr or Val
; US-10-379-392-139

Query Match          100.0%; Score 575; DB 16; Length 213;
Best Local Similarity 100.0%; Pred. No. 3.3e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTITCSASQDISNYLNMWYQKRGKAPKVLITYFTSSLHSGVPS 60
    |||
DB 1 DIQLTQSPSSLSASVGDRTITCSASQDISNYLNMWYQKRGKAPKVLITYFTSSLHSGVPS 60

QY 61 RFGSGSGTDFLTITISLQPEDPATYCCQYSTVPMWTFGQGTVEIKRTV 110
    |||
DB 61 RFGSGSGTDFLTITISLQPEDPATYCCQYSTVPMWTFGQGTVEIKRTV 110

RESULT 8
; US-10-364-953-1
; Sequence 1, Application US/10364953
; Publication No. US20030224397A1
; GENERAL INFORMATION:
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: NARVIN, JONATHAN S.
; TITLE OF INVENTION: ANTIBODY VARIANTS WITH FASTER ANTIGEN ASSOCIATION RATES
; FILE REFERENCE: P1951R1
; CURRENT APPLICATION NUMBER: US/10/364,953
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/355,895
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/409,685
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
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```

; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: Artificial sequence
; LOCATION: Full
; OTHER INFORMATION: Y0101-VL
; US-10-364-953-1

Query Match          100.0%; Score 575; DB 15; Length 214;
Best Local Similarity 100.0%; Pred. No. 3.4e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTITCSASQDISNYLNMWYQKRGKAPKVLITYFTSSLHSGVPS 60
    |||
DB 1 DIQLTQSPSSLSASVGDRTITCSASQDISNYLNMWYQKRGKAPKVLITYFTSSLHSGVPS 60

QY 61 RFGSGSGTDFLTITISLQPEDPATYCCQYSTVPMWTFGQGTVEIKRTV 110
    |||
DB 61 RFGSGSGTDFLTITISLQPEDPATYCCQYSTVPMWTFGQGTVEIKRTV 110

RESULT 9
; US-10-020-786-10
; Sequence 10, Application US/10020786
; Publication No. US20030073164A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Laura C.
; APPLICANT: Klimowski, Laura
; APPLICANT: Reilly, Dorothea
; APPLICANT: Yansura, Daniel G.
; TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
; FILE REFERENCE: P1793R1
; CURRENT APPLICATION NUMBER: US/10/020,786
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/256,164
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 10
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-VBGF light chain
; US-10-020-786-10

Query Match          100.0%; Score 575; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 3.7e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTITCSASQDISNYLNMWYQKRGKAPKVLITYFTSSLHSGVPS 60
    |||
DB 24 DIQLTQSPSSLSASVGDRTITCSASQDISNYLNMWYQKRGKAPKVLITYFTSSLHSGVPS 83

QY 61 RFGSGSGTDFLTITISLQPEDPATYCCQYSTVPMWTFGQGTVEIKRTV 110
    |||
DB 84 RFGSGSGTDFLTITISLQPEDPATYCCQYSTVPMWTFGQGTVEIKRTV 133

RESULT 10
; US-10-697-995-8
; Sequence 8, Application US/10697995
; Publication No. US20050048572A1
; GENERAL INFORMATION:
; APPLICANT: Reilly, Dorothea
; APPLICANT: Yansura, Daniel G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION
; FILE REFERENCE: 11669.195USU1
; CURRENT APPLICATION NUMBER: US/10/697,995
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: US 60/422,952
; PRIOR FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 8
; LENGTH: 237
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: anti-VEGF light chain
US-10-697-995-8

Query Match 100.0%; Score 575; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 3.7e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTSPSSLSASVGDRTVITCSASODISNLYNMYQOKPGKAPKVLIFTSSLSHGVS 60
DB 24 DIQLTSPSSLSASVGDRTVITCSASODISNLYNMYQOKPGKAPKVLIFTSSLSHGVS 83
QY 61 RFGSGSGTDFLTITLISLQPEDPATYCCQYSTVPMTFGGTVEIKRTV 110
DB 84 RFGSGSGTDFLTITLISLQPEDPATYCCQYSTVPMTFGGTVEIKRTV 133

RESULT 11
US-10-697-995-11
Sequence 11, Application US/10697995
Publication No. US20050048572A1
GENERAL INFORMATION:
APPLICANT: Reilly, Dorothea
APPLICANT: Yaneura, Daniel G.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION
FILE REFERENCE: 11669.195USU1
CURRENT APPLICATION NUMBER: US/10/697, 995
CURRENT FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: US 60/422,952
PRIOR FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 11
LENGTH: 237
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Anti-VEGF light chain
US-10-697-995-11

Query Match 100.0%; Score 575; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 3.7e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTSPSSLSASVGDRTVITCSASODISNLYNMYQOKPGKAPKVLIFTSSLSHGVS 60
DB 24 DIQLTSPSSLSASVGDRTVITCSASODISNLYNMYQOKPGKAPKVLIFTSSLSHGVS 83
QY 61 RFGSGSGTDFLTITLISLQPEDPATYCCQYSTVPMTFGGTVEIKRTV 110
DB 84 RFGSGSGTDFLTITLISLQPEDPATYCCQYSTVPMTFGGTVEIKRTV 133

RESULT 12
US-10-234-671-8
Sequence 8, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-10-234-671-8
SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Query Match 99.7%; Score 573; DB 14; Length 110;
Best Local Similarity 99.1%; Pred. No. 2.6e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTSPSSLSASVGDRTVITCSASODISNLYNMYQOKPGKAPKVLIFTSSLSHGVS 60
DB 1 DIQLTSPSSLSASVGDRTVITCSASODISNLYNMYQOKPGKAPKVLIFTSSLSHGVS 60
QY 61 RFGSGSGTDFLTITLISLQPEDPATYCCQYSTVPMTFGGTVEIKRTV 110
DB 61 RFGSGSGTDFLTITLISLQPEDPATYCCQYSTVPMTFGGTVEIKRTV 110

RESULT 13
US-10-624-153-94
Sequence 94, Application US/10624153
Publication No. US20040086502A1
GENERAL INFORMATION:
APPLICANT: CHEN, YVONNE M.
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MULLER, YVES
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469RIC1
CURRENT APPLICATION NUMBER: US/10/624,153
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 09/440,781
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: US 60/108,945
PRIOR FILING DATE: 1998-11-18
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 94
LENGTH: 110
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
NAME/KEY: artificial
LOCATION: 1-110
OTHER INFORMATION: humanized antibody light chain variable domain
US-10-624-153-94

Query Match 99.7%; Score 573; DB 15; Length 110;
Best Local Similarity 99.1%; Pred. No. 2.6e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGVDRVTITCSASQDISNYLNMWYQKPKAPKVLITYFTSSLSHGVP 60
Db 1 DIQLTQSPSSLSASVGVDRVTITCSASQDISNYLNMWYQKPKAPKVLITYFTSSLSHGVP 60

Qy 61 RFGSGSGGTDTFTLTSSLOPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 110
Db 61 RFGSGSGGTDTFTLTSSLOPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 110

RESULT 14
US-09-056-1608-105
Sequence 105, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:

APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056.1608

FILING DATE: 06-Apr-1998

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/054,856

FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: Haasek, Janet E.

REGISTRATION NUMBER: 28,616

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1896

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids

TYPE: Amino acid

TOPOLOGY: Linear

US-09-056-1608-105

Query Match 99.5%; Score 572; DB 9; Length 110;
Best Local Similarity 99.1%; Pred. No. 3.1e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGVDRVTITCSASQDISNYLNMWYQKPKAPKVLITYFTSSLSHGVP 60
Db 1 DIQLTQSPSSLSASVGVDRVTITCSASQDISNYLNMWYQKPKAPKVLITYFTSSLSHGVP 60

Qy 61 RFGSGSGGTDTFTLTSSLOPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 110
Db 61 RFGSGSGGTDTFTLTSSLOPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 110

RESULT 15
US-10-234-671-103

Sequence 103, Application US/100234671
Publication No. US20030190317A1
GENERAL INFORMATION:

APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/234,671

FILING DATE: 03-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/056160

FILING DATE: 06-Apr-1998

APPLICATION NUMBER: 60/126446

FILING DATE: 07-Apr-1997

APPLICATION NUMBER: 60/054856

FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 103:

SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids

TYPE: Amino acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 103:

US-10-234-671-103

Query Match 99.5%; Score 572; DB 14; Length 110;
Best Local Similarity 99.1%; Pred. No. 3.1e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGVDRVTITCSASQDISNYLNMWYQKPKAPKVLITYFTSSLSHGVP 60
Db 1 DIQLTQSPSSLSASVGVDRVTITCSASQDISNYLNMWYQKPKAPKVLITYFTSSLSHGVP 60

Qy 61 RFGSGSGGTDTFTLTSSLOPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 110
Db 61 RFGSGSGGTDTFTLTSSLOPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 110

Search completed: March 14, 2005, 20:42:12
Job time: 41.0086 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: March 14, 2005, 20:39:29 ; Search time 16.6447 Seconds
(without alignments)
635.867 Million cell updates/sec

Title: US-09-723-752b-115
Perfect score: 575
Sequence: 1 DIQLTQSPSSLSASVGDRTV.....YSTVPWTFGGTKVETIKRTV 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	510	88.7	127	2 S40367	Ig kappa chain V-J
2	487	84.7	108	1 K1HUNU	Ig kappa chain V-I
3	483	84.0	125	2 S40333	Ig kappa chain V-J
4	482	83.8	123	2 S40331	Ig kappa chain - h
5	481	83.7	108	2 B49047	Ig kappa chain V r
6	479	83.3	131	2 S40352	Ig kappa chain V-J
7	479	83.3	108	2 S44132	Ig kappa chain V r
8	479	83.3	109	2 S31998	Ig kappa chain - h
9	477	83.0	107	2 S36264	Ig lambda chain V
10	477	83.0	129	2 S52789	Ig kappa chain V r
11	473.5	82.3	124	2 S40336	Ig kappa chain V-J
12	473	82.3	129	2 S40359	Ig kappa chain - h
13	471	81.9	108	1 K1HUNU	Ig kappa chain V-I
14	470	81.7	108	2 S19674	Ig kappa chain V r
15	470	81.7	132	2 S40334	Ig kappa chain - h
16	469	81.6	108	1 K1HUNE	Ig kappa chain V-I
17	469	81.6	119	2 S31981	Ig kappa chain - h
18	469	81.6	111	2 A38740	Ig kappa chain V r
19	469	81.6	125	2 S40349	Ig kappa chain V-J
20	467	81.2	110	2 S44118	Ig kappa chain V-J
21	466	81.0	108	1 K1HUNE	Ig kappa chain V-I
22	466	81.0	139	2 S40365	Ig kappa chain - h
23	465.5	81.0	107	2 S36275	Ig lambda chain V
24	464	80.7	108	1 K1HUNG	Ig kappa chain V-I
25	464	80.7	108	1 K1HUNB	Ig kappa chain V-I
26	463	80.5	108	2 S47182	Ig kappa chain - h
27	463	80.5	130	2 S40366	Ig kappa chain - h
28	462	80.3	125	2 S40316	Ig kappa chain - h
29	461	80.2	108	2 I39154	Ig kappa chain (BR

30	461	80.2	111	2 E38740	Ig kappa chain V r
31	461	80.2	122	2 S40370	Ig kappa chain - h
32	459	79.8	108	1 K1HUNE	Ig kappa chain V-I
33	459	79.8	111	2 C38740	Ig kappa chain V r
34	459	79.8	122	2 S40314	Ig kappa chain - h
35	459	79.8	129	2 S40317	Ig kappa chain V r
36	459	79.8	129	2 S52793	Ig kappa chain pre
37	459	79.8	135	2 S24320	Ig kappa chain V r
38	458	79.7	107	2 I69017	Ig kappa chain - h
39	457.5	79.6	125	2 S40315	Ig kappa chain V
40	457	79.5	107	2 S36269	Ig kappa chain V-J
41	457	79.5	117	2 S46371	Ig kappa chain pre
42	457	79.5	129	1 K1HUNK	Ig kappa chain V r
43	456	79.3	111	2 G38740	Ig kappa chain V r
44	456	79.3	117	2 S46376	Ig kappa chain V-J
45	456	79.3	128	2 S46372	Ig kappa chain var

ALIGNMENTS

RESULT 1
S40367
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40367
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40367
A/Status: preliminary; translation not shown
A/Structure: preliminary
A/Molecule type: mRNA
A/Residues: 1-127 <KLE>
A/Cross-references: EMBL:X72477
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 88.7%; Score 510; DB 2; Length 127;
Best Local Similarity 89.1%; Score No. 5, 3e-38;
Matches 98; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVTTTCSASQDTSNTLNWYQKRGKAPKVLIVTSSLSHGVP 60
DB 18 DIQMTQSPSSLSASVGDRTVITCRASQISNTLNWYQKRGKAPKLVIAASSLSQGVPS 77
QY 61 RFSGSGSGTDFTLTISLSLOPEDPATYCCQYSTVPWTFGGTKVETIKRTV 110
DB 78 RFSGSGSGTDFTLTISLSLOPEDPATYCCQSYNTPTTFGGTKVETIKRTV 127

RESULT 2

K1HUNU
Ig kappa chain V-I region (Au) - human
C/Species: Homo sapiens (man)
C/Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C/Accession: A91653; A01862; S02573
R/Schleichl, H.; Physiol. Chem. 353, 345-370, 1972
Hoppe-Seyler's Z. Physiol. Chem.
A/Title: Die Primärstruktur einer monoklonalen Immunoglobulin-L-Kette vom kappa-Typ, Su
A/Reference number: A91653; MUID:72189444; PMID:5028201
A/Accession: A91653
A/Molecule type: protein
A/Residues: 1-108 <SCH>
A/Cross-references: UNIPROT:P01594
A/Note: the C region of this chain has the Inv (3) marker
R/Fellhammer, H.; Schiffer, M.; Bep, O.; Colman, P.M.; Lettman, E.E.; Schwager, P.; Ste
Biophys. Struct. Mech. 1, 139-146, 1975
A/Title: The structure determination of the variable portion of the Bence-Jones protein
A/Reference number: A90729; MUID:77022433; PMID:11234024
A/Contents: annotation; X-ray crystallography

R./Klein, R.; Juenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chl genes and their hypermutation
A/Reference number: 840312: MIMD:94080891: PMID:8258341

A/Residues: 1-131 <LE>
A/Cross-references: EMBL:X72462; NID:g441392; PIDN:CAAS1130.1; PID:g441392
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40336
 R/Klein, R.; Jaenichen, H. G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40332; MUID:94080891; PMID:8258341
 A/Accession: S40336
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-124 <KLE>
 A/Cross-references: EMBL:X72446; NID:G441360; PIDN:CAAS114.1; PID:G441361
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F,31-105/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 473.5; DB 2; Length 124;
 Best Local Similarity 85.3%; Pred. No. 8.3e-35;
 Matches 93; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGRVTITCSASQDISNYLWYQKPGKAPKVLITYFTSSLHSGVPS 60
 |||||
 Db 16 DIQLTQSPSSLSASVGRVTITCRASQGISYLAWYQKPGKAPKVLITYAASLQSGVPS 75
 Qy 61 RFSSGSGGTDFTLTITSLQPEDFATYCCQYSTV-PWTFGGGTKEIKR 108
 |||||
 Db 76 RFSSGSGGTDFTLTITSLQPEDFATYCCQQLNTYPPWTFGGGTKEIKR 124

RESULT 12

S40369
 Ig kappa chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40369
 R/Klein, R.; Jaenichen, H. G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40369
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-129 <KLE>
 A/Cross-references: EMBL:X72479; NID:G441426; PIDN:CAAS114.1; PID:G441427
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F,37-111/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 473; DB 2; Length 129;
 Best Local Similarity 84.3%; Pred. No. 9.6e-35;
 Matches 91; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGRVTITCSASQDISNYLWYQKPGKAPKVLITYFTSSLHSGVPS 60
 |||||
 Db 22 DIQLTQSPSSLSASVGRVTITCRASHVISNHLVWFQKPGKAPKVLITYAASLQSGVPS 81
 Qy 61 RFSSGSGGTDFTLTITSLQPEDFATYCCQYSTVWTFGGGTKEIKR 108
 |||||
 Db 82 RFSSGSGGTDFTLTITSLQPEDFATYCCQYNSYPTFGGGTKEIKR 129

RESULT 13

K1RHU
 Ig kappa chain V-I region (Hau) - human
 C/Species: Homo sapiens (man)
 C/Date: 24-Apr-1994 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
 C/Accession: A01868; S02574
 R/Matambes, S.; Hilschmann, N.
 Hope-Seyler's Z. Physiol. Chem. 351, 1291-1295, 1970
 A>Title: The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subg
 A/Reference number: A01868; MUID:71032830; PMID:4097974
 A/Molecule type: protein
 A/Residues: 1-108 <MAT>

A/Cross-references: UNIPROT:P01600
 A/Note: The C region of this chain has the Inv (3) marker
 R/Steiner, V.; Chang, J. Y.
 FEBS Lett. 222, 6-10, 1987
 A>Title: Chemical modification of the carboxyl groups of protein substrates enhances th
 A/Reference number: S02572; MUID:88005152; PMID:3115831
 A/Contents: annotation
 C/Comment: This is a Bence Jones protein.
 C/Genetics:
 A/Gene: GDB:IGKV1
 A/Cross-references: GDB:136264
 A/Map position: 2p12-2p12
 C/Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kai
 hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into 1;
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F,16-90/Domain: immunoglobulin homology <IMM>
 F,23-88/Domain: heterotetramer predicted

Query Match 81.9%; Score 471; DB 1; Length 108;
 Best Local Similarity 85.2%; Pred. No. 1.2e-34;
 Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGRVTITCSASQDISNYLWYQKPGKAPKVLITYFTSSLHSGVPS 60
 |||||
 Db 1 DIQLTQSPSSLSASVGRVTITCRASQGISYLAWYQKPGKAPKVLITYAASLQSGVPS 60
 Qy 61 RFSSGSGGTDFTLTITSLQPEDFATYCCQYSTVWTFGGGTKEIKR 108
 |||||
 Db 61 RFSSGSGGTDFTLTITSLQPEDFATYCCQNYIYPTFGGGTKEIKR 108

RESULT 14

S19674
 Ig kappa chain V region (clone alpha-TEL9) - human
 C/Species: Homo sapiens (man)
 C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
 C/Accession: S19674
 R/Marks, J. D.; Hoogenboom, H. R.; Bonnett, T. P.; McCafferty, J.; Griffiths, A. D.; Winter, J. M.
 J. Mol. Biol. 222, 581-597, 1991
 A>Title: By-passing immunization. Human antibodies from V-gene libraries displayed on p
 A/Reference number: S19663; MUID:92085276; PMID:1748994
 A/Accession: S19674
 A/Molecule type: mRNA
 A/Residues: 1-108 <MKR>
 A/Cross-references: EMBL:X61642; NID:G37860; PIDN:CA43823.1; PID:G1335386
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F,16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 470; DB 2; Length 108;
 Best Local Similarity 84.3%; Pred. No. 1.5e-34;
 Matches 91; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGRVTITCSASQDISNYLWYQKPGKAPKVLITYFTSSLHSGVPS 60
 |||||
 Db 1 EIVLTQSPSSLSASVGRVTITCRASQDISNYLWYQKPGKAPKVLITYAASLQSGVPS 60
 Qy 61 RFSSGSGGTDFTLTITSLQPEDFATYCCQYSTVWTFGGGTKEIKR 108
 |||||
 Db 61 RFSSGSGGTDFTLTITSLQPEDFATYCCQNTSFPWTFGGGTKEIKR 108

RESULT 15

S40334
 Ig kappa chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40334
 R/Klein, R.; Jaenichen, H. G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40334
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-132 <KLB>
A/Cross-references: EMBL:X72444
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/37-111/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 470; DB 2; Length 132;
Best Local Similarity 80.9%; Pred. No. 1.8e-34;
Matches 89; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

Qy	1	DIQLTQSPFSLASAVGDRVTITCSASQDISNLYLMTYQKPKAPKVLITYFTSLHSGVPS	60
Db	22	DIQLTQSPFSLASIGDRVTITCRASQGINSLAWYQKPKAPKLLIYVASTLQSGVPS	81
Qy	61	RPSGSGSGTDFTLTISLQPEDPATYCCQYSTVPTFGQTKVEIKRTV	110
Db	82	RPSGSGSGTEFTLTISLQPEDPASYYCQPFNSYPTFGGTVKVEIRRTV	131

Search completed: March 14, 2005, 21:08:52
JOB time : 17.6447 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 14, 2005, 20:32:33 ; Search time 77.193 Seconds
(without alignments)
729.713 Million cell updates/sec

Title: US-09-723-752B-115

Perfect score: 575
Sequence: 1 DIQLTQSPSSLSASVCDRYT.....YSTVPWFPGQIKVEIKRTV 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	487	84.7	108	1 KVI1B_HUMAN	P01594 homo sapien
2	485	84.3	108	2 Q9UL77	Q9UL77 homo sapien
3	483	84.0	236	2 Q6GMX9	Q6GMX9 homo sapien
4	482	83.8	236	2 Q6GMW1	Q6GMW1 homo sapien
5	481	83.7	236	2 Q7Z3Y4	Q7Z3Y4 homo sapien
6	474.5	82.5	107	2 Q96S89	Q96S89 homo sapien
7	474	82.4	236	2 Q6GMX8	Q6GMX8 homo sapien
8	471	81.9	108	1 KVI1H_HUMAN	P01600 homo sapien
9	471	81.9	108	1 KVI1Y_HUMAN	P01602 homo sapien
10	471	81.9	236	2 Q6GMX0	Q6GMX0 homo sapien
11	469	81.6	108	1 KVI1R_HUMAN	P01610 homo sapien
12	466	81.0	108	1 KVI1O_HUMAN	P01607 homo sapien
13	465	80.9	108	2 Q9UL70	Q9UL70 homo sapien
14	465	80.9	236	2 Q6PIH7	Q6PIH7 homo sapien
15	464	80.7	108	1 KVI1A_HUMAN	P01593 homo sapien
16	464	80.7	108	1 KVI1V_HUMAN	P04430 homo sapien
17	462	80.3	234	2 Q7Z473	Q7Z473 homo sapien
18	459	79.8	108	1 KVI1P_HUMAN	P01608 homo sapien
19	457	79.5	129	1 KVI1W_HUMAN	P04431 homo sapien
20	455	79.1	108	1 KVI1E_HUMAN	P01597 homo sapien
21	454.5	79.0	107	1 KVI1D_HUMAN	P01596 homo sapien
22	454	79.0	108	1 KVI1M_HUMAN	P01605 homo sapien
23	453	78.8	108	1 KVI1K_HUMAN	P01603 homo sapien
24	452.5	78.7	107	2 Q9UL81	Q9UL81 homo sapien
25	452	78.6	244	2 Q6SZC8	Q6SZC8 homo sapien
26	449	78.1	108	1 KVI1Q_HUMAN	P01609 homo sapien
27	448	77.9	108	1 KVI1J_HUMAN	P01611 homo sapien
28	448	77.9	116	2 Q96PF6	Q96PF6 homo sapien
29	447	77.7	108	1 KVI1N_HUMAN	P01606 homo sapien
30	446	77.6	108	1 KVI1C_HUMAN	P01595 homo sapien
31	445	77.4	108	1 KVI5J_MOUSE	P01643 mus musculi

32	445	77.4	236	2 Q6PIT5	Q6PIT5 homo sapien
33	445	77.4	240	2 Q6SZC9	Q6SZC9 homo sapien
34	443	77.0	108	1 KVI1G_HUMAN	P01599 homo sapien
35	439	76.3	108	1 KVI1F_HUMAN	P01598 homo sapien
36	439	76.3	108	1 KVI1L_HUMAN	P01604 homo sapien
37	439	76.3	108	2 Q9UL79	Q9UL79 homo sapien
38	438	76.2	236	2 Q6PIH4	Q6PIH4 homo sapien
39	428	74.4	108	1 KVSJ_MOUSE	P01644 mus musculi
40	428	74.4	108	1 KVSJ_MOUSE	P01647 mus musculi
41	426	74.1	108	1 KVSJ_MOUSE	P01645 mus musculi
42	426	74.1	108	1 KVSJ_MOUSE	P01646 mus musculi
43	425	73.9	108	1 KVSJ_MOUSE	P01648 mus musculi
44	424.5	73.8	109	1 KVI1T_HUMAN	P01612 homo sapien
45	422	73.4	108	1 KVSU_MOUSE	P01946 mus musculi

ALIGNMENTS

RESULT 1	ID	KVI1B_HUMAN	STANDARD,	PRT,	108 AA.
AC	P01594;				
AD	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Ig kappa chain V-1 region AU.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=72189444; PubMed=5028201;				
RA	Schleich H., Hilschmann N.;				
RT	"Rule of antibody structure. The primary structure of a monoclonal				
RT	immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones				
RT	protein Au).";				
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).				
RN	[2]				
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).				
RX	MEDLINE=77022433; PubMed=1234024;				
RA	Fehlhammer H., Schiffer M., Bpp O., Colman P.M., Lattman B.E.,				
RT	Schwager P., Steigemann W., Schramm H.J.;				
RT	"The structure determination of the variable portion of the Bence-				
RT	Jones protein Au.";				
RL	Biophys. Struct. Mech. 1:139-146(1975).				
CC	-I- MISCELLANEOUS: The structure of the V region was determined by				
CC	molecular replacement using the known structure of the V				
CC	region of the kappa chain R1.				
CC	-I- MISCELLANEOUS: This is a Bence-Jones protein.				
CC	PDB; 1JVS; X-ray; A=1-107.				
DR	GO; GO:0005576; C:extracellular; NAS.				
DR	GO; GO:0003823; P:antigen binding; NAS.				
DR	GO; GO:0006955; P:immune response; NAS.				
DR	InterPro; IPR007110; IG-like.				
DR	InterPro; IPR003596; IG_V.				
DR	Pfam; PF00047; IG_1.				
DR	SMART; SM00406; IGV_1.				
DR	PROSITE; PS00835; IG_LIKE; 1.				
KW	3D-structure; Bence-Jones protein; Direct protein sequencing;				
KW	Immunoglobulin V region.				
FT	DOMAIN 1 23				
FT	DOMAIN 24 34				
FT	DOMAIN 35 49				
FT	DOMAIN 50 56				
FT	DOMAIN 57 88				
FT	DOMAIN 89 97				
FT	DOMAIN 98 107				
FT	DISULFID 23 88				
FT	STRAND 4 5				

Framework-1.
Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
Framework-3.
Complementarity-determining-3.
Framework-4.
By similarity.

```
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT STRAND 60 61
FT TURN 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187EB6FEFB9 CRC64;

Query Match 84.7%; Score 487; DB 1; Length 108;
Best Local Similarity 85.2%; Pred. No. 2,3e-42;
Matches 92; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

1 DIQITQSPSSLSASVGRVTTTCASQDISNYLNMVQOKPGKAPKVLIIYFTSSLSHGVP 60
1 DIQMTQSPSSLSASVGRVTTTCASQDISNYLNMVQOKPGKAPKVLIIYFTSSLSHGVP 60

Db 61 RFSGSGSGTDFTLTISLQPEDFATVYCOQYSTVPMWTFGQTKVEIKR 108
61 RFSGSGSGAGHFTTISLQPEDIATVYCOQYDYLPMWTFGQTKVEIKR 108

RESULT 2
ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus ";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; 1BWM.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV_1.
DR SMART; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 84.3%; Score 485; DB 2; Length 108;
Best Local Similarity 86.1%; Pred. No. 3,8e-42;
Matches 93; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

1 DIQITQSPSSLSASVGRVTTTCASQDISNYLNMVQOKPGKAPKVLIIYFTSSLSHGVP 60
1 DIQMTQSPSSLSASVGRVTTTCASQDISNYLNMVQOKPGKAPKVLIIYFTSSLSHGVP 60
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Db 1 DIQMTQSPSSLSASVGRVTTTCASQDISNYLNMVQOKPGKAPKVLIIYFTSSLSHGVP 60
Qy 61 RFSGSGSGTDFTLTISLQPEDFATVYCOQYSTVPMWTFGQTKVEIKR 108
61 RFSGSGSGTDFTLTISLQPEDFATVYCOQYSTVPMWTFGQTKVEIKR 108

Db 61 RFSGSGSGTDFTLTISLQPEDFATVYCOQYSTVPMWTFGQTKVEIKR 108

RESULT 3
ID Q6GMX9 PRELIMINARY; PRT; 236 AA.
AC Q6GMX9;
DT 05-JUN-2004 (Tremblrel. 27, Created)
DT 05-JUN-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUN-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhac N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Ditchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavini T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshivuki S., Carinini P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holly S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences ";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; -.
DR InterPro; IPR003599; IG_1like.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003066; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-sect; 1.
DR Pfam; PF00047; Ig; 2.
DR Pfam; SM00409; Ig; 2.
DR SMART; SM00407; IGV_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25924 MW; FBE2093DC560CF7 CRC64;

Query Match 84.0%; Score 483; DB 2; Length 236;
Best Local Similarity 85.5%; Pred. No. 1,5e-47;
Matches 94; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

1 DIQITQSPSSLSASVGRVTTTCASQDISNYLNMVQOKPGKAPKVLIIYFTSSLSHGVP 60
1 DIQMTQSPSSLSASVGRVTTTCASQDISNYLNMVQOKPGKAPKVLIIYFTSSLSHGVP 60
23 DIQMTQSPSSLSASVGRVTTTCASQDISNYLNMVQOKPGKAPKVLIIYFTSSLSHGVP 82
61 RFSGSGSGTDFTLTISLQPEDFATVYCOQYSTVPMWTFGQTKVEIKR 110
```

DB 83 RFGSGSGTDFLTITLISLOPEDFATYCCQGYNTYPLFGGTGKVEIKRTV 132

RESULT 4

06GMM1 PRELIMINARY; PRT; 236 AA.
 AC 06GMM1; 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywiński M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Spleen;
 RC Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073791; AAH73791.1; -
 DR InterPro: IPR003599; IG_1like.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_1like.
 DR InterPro: IPR003596; IG_1like.
 DR InterPro: IPR003596; IG_1like.
 DR Pfam; PF07654; Cl-sec; 1.
 DR Pfam; PF00047; IG_2.
 DR SMART; SM00409; IG_2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PSS0835; IG_1like; 2.
 DR PROSITE; PSS0290; IG_MHC; 1.
 DR Hypothetical protein.
 KM SEQUENCE 236 AA; 25751 MW; 58F6A087AFAC437 CRC64;
 Query Match 83.8%; Score 482; DB 2; Length 236;
 Best Local Similarity 87.2%; Pred. No. 1.9e-41;
 Matches 95; Conservative 2; Mismatches 12; Indels 0; Gaps 0;
 QY 2 IQLTQSSSLASVGVDRVTITCSASODISNLYLWYQKRGKAPKYLITFTSLHSGVPSR 61
 DB 24 IQMTQSSSLASVGVDRVTITCRASQGISNDLGWYQKRGKAPKYLITFTSLHSGVPSR 83
 QY 62 FSGSGSGTDFLTITLISLOPEDFATYCCQGYNTYPLFGGTGKVEIKRTV 110
 DB 84 FSGSGSGTDFLTITLISLOPEDFATYCCQGYNTYPLFGGTGKVEIKRTV 132

RESULT 5

0723Y4 PRELIMINARY; PRT; 236 AA.
 AC 0723Y4; 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal Muscle;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywiński M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Skeletal Muscle;
 RC Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005332; AAH05332.1; -
 DR HSP; P01834; 1HEZ.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_1like.
 DR InterPro: IPR003596; IG_1like.
 DR InterPro: IPR003596; IG_1like.
 DR Pfam; PF07654; Cl-sec; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PSS0835; IG_1like; 2.
 DR PROSITE; PSS0290; IG_MHC; 1.
 DR Hypothetical protein.
 KM SEQUENCE 236 AA; 25702 MW; 7FBFB4BD23084BC6 CRC64;
 Query Match 83.7%; Score 481; DB 2; Length 236;
 Best Local Similarity 85.5%; Pred. No. 2.4e-41;
 Matches 94; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 DIQLTQSSSLASVGVDRVTITCSASODISNLYLWYQKRGKAPKYLITFTSLHSGVPS 60
 DB 23 DIQLTQSSSLASVGVDRVTITCRASQGISNDLGWYQKRGKAPKYLITFTSLHSGVPS 82
 QY 61 RFGSGSGTDFLTITLISLOPEDFATYCCQGYNTYPLFGGTGKVEIKRTV 110
 DB 83 RFGSGSGTDFLTITLISLOPEDFATYCCQGYNTYPLFGGTGKVEIKRTV 132
 RESULT 6
 QY 096SA9 PRELIMINARY; PRT; 107 AA.
 AC 096SA9;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
 DE variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RX MEDLINE=98375893; PubMed=9712075;
 RA "Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
 RT "Molecular analysis of polyclonal monoclonal antibodies from
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
 RT antibody V region genes.";
 RL J. Immunol. 161:2020-2031(1998).
 DR EMBL; U96396; AAB6785.1; -
 DR PIR; B49047; B49047.
 DR PIR; PH0867; PH0867.
 DR PIR; S16840; S16840.
 DR PIR; S31977; S31977.
 DR PIR; S34083; S34083.
 DR PIR; S34086; S34086.
 DR HSP; P01607; 1BWW.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 107
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;

Query Match 82.5%; Score 474.5; DB 2; Length 107;
 Best Local Similarity 88.1%; Pred. No. 4.5e-41;
 Matches 96; Conservative 4; Mismatches 6; Indels 3; Gaps 2;
 QY 1 DIQLTQSPSSLSASVGRVITITCSASODISNYLNMVYQKPKGAPKVLITFTSSLSHGVS 60
 DB 1 DIQLTQSPSSLSASVGRVITITCRASQGISSTLNMVYQKPKGAPKVLITFTSSLSHGVS 60
 QY 61 RFSGSGSGTDFLTITSLTSLQPEDPATYTCQYSTVPTVFGGCTVKEIRK 108
 DB 61 RFSGSGSGTDFLTITSLTSLQPEDPATYTCQYSTVPTVFGGCTVKEIRK 107

RESULT 7
 Q6GMX8 PRELIMINARY; PRT; 236 AA.
 AC Q6GMX8;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RX MEDLINE=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Steplowitz M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Cantini P., Pange C.,
 RA Raba S.S., Loguanello N.A., Peters G.J., Abrahamson R.D., Mullahy S.J.,
 RA Boeck S.A., McBreen P.J., McKernan K.J., Malik J.A., Gunaratne P.H.,
 RA Richards S., Morley C.C., Hale S., Garcia A.W., Gay L.J., Huijck S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RX MEDLINE=11032830; PubMed=1097974;
 RA Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
 RT subgroup.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A01688; K1H0H0.
 DR PDB; 1F6L; X-ray; L=1-108.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0005855; P:immune response; NAS.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 SQ SEQUENCE 236 AA; 25707 MW; 4FCBE14B6559EFC9 CRC64;

Query Match 82.4%; Score 474; DB 2; Length 236;
 Best Local Similarity 83.6%; Pred. No. 1.3e-40;
 Matches 92; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLSASVGRVITITCSASODISNYLNMVYQKPKGAPKVLITFTSSLSHGVS 60
 DB 23 DIQLTQSPSSLSASVGRVITITCRASQGISSTLNMVYQKPKGAPKVLITFTSSLSHGVS 82
 QY 61 RFSGSGSGTDFLTITSLTSLQPEDPATYTCQYSTVPTVFGGCTVKEIRK 110
 DB 83 RFSGSGSGTDFLTITSLTSLQPEDPATYTCQYSTVPTVFGGCTVKEIRK 132

RESULT 8
 KVIH_HUMAN STANDARD; PRT; 108 AA.
 ID KVIH_HUMAN
 AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig kappa chain V-I region Hau.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RX MEDLINE=71032830; PubMed=1097974;
 RA Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
 RT subgroup.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A01688; K1H0H0.
 DR PDB; 1F6L; X-ray; L=1-108.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0005855; P:immune response; NAS.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.

DR PROSITE; PS50835; IG LIKE; 1.
 KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
 FT Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Complementarity-determining-2.
 FT DOMAIN 50 56 Complementarity-determining-3.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Framework-4.
 FT DISULFID 98 107 By similarity.
 FT NON TER 23 88
 FT SEQUENCE 108 AA; 11671 MW; 08D3A6160DB0618 CRC64;
 SO
 Query Match 81.9%; Score 471; DB 1; Length 108;
 Best Local Similarity 85.2%; Pred. No. 1e-40;
 Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLSASVGDRTITCSASODISNLYNMWQKRGKAPKLYIFTSSLSHGVP 60
 DB 1 DIQLTQSPSSLSASVGDRTITCRASQSISSYLSWYQKRGKAPQVLYIYASSLPSGVP 60
 QY 61 RFSGSGSGTDFLTITSSLOPEDFATYCCQYSTVPTFGGTKEIKR 108
 DB 61 RFSGSGSGTDFLTITSSLOPEDFATYCCQYITFTSFSGGTKEIKR 108
 SO
 RESULT 9
 ID KVLV HUMAN STANDARD; PRT; 108 AA.
 AC P80362;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig kappa chain V-J region MAT.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI TaxID=9606;
 RN
 RP SEQUENCE AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=95086080; PubMed=7993911;
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
 RA Solomon A., Stevens F.J., Schiffer M.;
 RT "Comparison of crystal structures of two homologous proteins:
 RT structural origin of altered domain interactions in immunoglobulin
 RT light-chain dimers.";
 RT J. Biochem. 147:185-193(1981).
 RL J. Mol. Biol. 147:185-193(1981).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PDB; 1WTU; X-ray; A/B=1-108.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KM 3D-structure; Bence-Jones protein; Direct protein sequencing;
 FT Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Complementarity-determining-2.
 FT DOMAIN 50 56 Complementarity-determining-3.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Framework-4.
 FT DISULFID 98 107 By similarity.
 FT NON TER 23 88
 FT SEQUENCE 108 AA; 11671 MW; 08D3A6160DB0618 CRC64;
 SO

FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT CONFLICT 30 31 TN -> SD (in Ref. 2).
 FT STRAND 4 7
 FT STRAND 10 13
 FT STRAND 15 16
 FT STRAND 19 25
 FT STRAND 30 31
 FT STRAND 33 38
 FT STRAND 40 41
 FT STRAND 45 49
 FT STRAND 50 52
 FT STRAND 53 54
 FT STRAND 56 57
 FT STRAND 62 67
 FT STRAND 68 69
 FT STRAND 70 75
 FT STRAND 80 82
 FT STRAND 84 90
 FT STRAND 98 98
 FT STRAND 102 106
 FT NON TER 108 108
 SO SEQUENCE 108 AA; 11737 MW; D9D341B3F0FAE697 CRC64;
 Query Match 81.9%; Score 471; DB 1; Length 108;
 Best Local Similarity 82.4%; Pred. No. 1e-40;
 Matches 89; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLSASVGDRTITCSASODISNLYNMWQKRGKAPKLYIFTSSLSHGVP 60
 DB 1 DIQLTQSPSSLSASVGDRTITCRASQDIYVNMWQKRGKAPKLYIGASTLETGVP 60
 QY 61 RFSGSGSGTDFLTITSSLOPEDFATYCCQYSTVPTFGGTKEIKR 108
 DB 61 RFSGSGSGTDFLTITSSLOPEDFATYCCQYITFTSFSGGTKEIKR 108
 SO
 RESULT 10
 ID O6GKXO PRELIMINARY; PRT; 236 AA.
 AC O6GKXO;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI TaxID=9606;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.U., Uvedit T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 RA Bosek S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Rahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Skladow J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Spleen;
 RA Straussberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC073775; AAH73775.1; -.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-sec; 1.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PSS0835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR Hypothetical protein.
 KW SEQUENCE 236 AA; 25807 MW; 864EA08C7E2BF8F CRC64;

Query March 81.9%; Score 471; DB 2; Length 236;
 Best Local Similarity 82.7%; Pred.No. 2.6e-40;
 Matches 91; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDVVTITCSASQDISNYLNMVYQOKPKAPKVLITYFTSSLSHGVS 60
 DB 23 DIQMTQSPSSLSASVGDVVTITCSASQINNNYLMYQOKPKAPKVLITYFTSSLSHGVS 82
 QY 61 RFSGSGSGTDFTLTISLTQPEDFATYYCOQYSTVPMWFGQGTVEIKRTV 110
 DB 83 RFSGSGSGTDFTLTISLTQPEDFATYYCOQSYNIPLTFGGGWEIKRTV 132

RESULT 11
 ID_KVIR_HUMAN STANDARD; PRT; 108 AA.
 AC P01610;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE IG kappa chain V-I region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NX NCBI_TaxID=9606;
 RP [1]
 RN SEQUENCE.
 RX MEDLINE=83273707; PubMed=6410398;
 RA Goni F., Frangione B.;
 RT "Antibody acid sequence of the Fv region of a human monoclonal IGM
 (protein WEA) with antibody activity against 3,4-pyruvylated galactose
 in Klebsiella polysaccharides K30 and K33."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).
 CC -1- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
 against 3,4-pyruvylated galactose and isolated from a patient with
 Waldenstrom's macroglobulinemia.
 DR PIR; A01876; KIHUME.
 DR HSSP; P80362; IWTU.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region;
 KM Monoclonal antibody.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.

FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query March 81.6%; Score 469; DB 1; Length 108;
 Best Local Similarity 83.3%; Pred.No. 1.7e-40;
 Matches 90; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDVVTITCSASQDISNYLNMVYQOKPKAPKVLITYFTSSLSHGVS 60
 DB 1 DIQMTQSPSSLSASVGDVVTITCSASQINNNYLMYQOKPKAPKVLITYFTSSLSHGVS 60
 QY 61 RFSGSGSGTDFTLTISLTQPEDFATYYCOQYSTVPMWFGQGTVEIKR 108
 DB 61 RFSGSGSGTDFLTISLTQPEDFATYYCLOYSFPMWFGQGTVEIKR 108

RESULT 12
 ID_KVIO_HUMAN STANDARD; PRT; 108 AA.
 AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE IG kappa chain V-I region Rel.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NX NCBI_TaxID=9606;
 RP [1]
 RN SEQUENCE.
 RX MEDLINE=76033758; PubMed=809329;
 RA Palm W., Hilschmann N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin
 kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
 and characterization of the tryptic peptides; the complete amino acid
 sequence of the protein; a contribution to the elucidation of the
 three-dimensional structure of antibodies, in particular their
 combining site."
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191 (1975).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=76039968; PubMed=1182131;
 RA Bep O., Iatman E.B., Schiffer M., Huber R., Palm W.;
 RT "The molecular structure of a dimer composed of the variable portions
 of the Bence-Jones protein RFI refined at 2.0-A resolution."
 RL Biochemistry 14:4943-4952 (1975).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A9163; KIHUME.
 DR PDB; 1AR2; X-ray; @=1-107.
 DR PDB; 1BMW; X-ray; A/B=1-107.
 DR PDB; 1REI; X-ray; A/B=1-107.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.


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FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88
FT STRAND 4 7
FT TURN 10 13
FT TURN 15 16
FT TURN 19 25
FT TURN 30 31
FT TURN 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 988143E1188BCE2A CRC64;

Query Match 81.0%; Score 466; DB 1; Length 108;
Best Local Similarity 80.6%; Pred. No. 3,4e-40;
Matches 87; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIDLQSPSSLSASVGDRTVITTCASODISNYLNMWYQOKRKPVLITFTSSLHSGVPS 60
Db 1 DIDLQSPSSLSASVGDRTVITTCASODISNYLNMWYQOKRKPVLITFTSSLHSGVPS 60

Qy 61 RFGSGSGTDFLTITSLQPEDFATYVCOQYSTVPMTFGQGTVEIKR 108
Db 61 RFGSGSGTDFLTITSLQPEDFATYVCOQYSTVPMTFGQGTVEIKR 108

RESULT 13
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Werpe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AA056280.1; -.
DR PIR; P08633; P08633.
DR HSP; P01607; I8MW.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 108 108
FT SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 80.9%; Score 465; DB 2; Length 108;
Best Local Similarity 83.3%; Pred. No. 4.3e-40;
Matches 83; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

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Matches 90; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 DIDLQSPSSLSASVGDRTVITTCASODISNYLNMWYQOKRKPVLITFTSSLHSGVPS 60
Db 1 DIDLQSPSSLSASVGDRTVITTCASODISNYLNMWYQOKRKPVLITFTSSLHSGVPS 60

Qy 61 RFGSGSGTDFLTITSLQPEDFATYVCOQYSTVPMTFGQGTVEIKR 108
Db 61 RFGSGSGTDFLTITSLQPEDFATYVCOQYSTVPMTFGQGTVEIKR 108

RESULT 14
Q6PIH7 PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Burow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heise F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin C.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalka U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Warr M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Straubeberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AA034141.1; -.
DR HSP; P01607; IAR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_CL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-sev; 1.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGCL1; 1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match 80.9%; Score 465; DB 2; Length 236;
Best Local Similarity 83.4%; Pred. No. 1.1e-39;
Matches 92; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

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Db      23 DIQLTQSPFSLASVGDRTITCRASQGISSTLANIYQKPKAPNLLIYASTLQSGVPS 82
Qy      61 RFGSGSGCTDFLTLLTISLQPEDFATYCCQYSTVPTFGQGTKEIKRTV 110
Db      83 RFGSGSGCTEFTLLTISLQPEDFATYCCQQLNSPPTFGGKTKEIKRTV 132

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RESULT 15

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KVIA_HUMAN          STANDARD;          PRT;          108 AA.
ID   P01593
AC   P01593
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-I region AG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX   NCBI_TaxID=9606;
RX   MEDLINE=69234734; PubMed=4893682;
RA   Tlicani K., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT   complete sequence and the location of the disulfide bridges."
RL   J. Biol. Chem. 244:3550-3560(1969).
CC   -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR: A01861; KIHUAG.
DR   HSP: P01607; 1BWV.
DR   GO: GO:0005576; C:extracellular; NAS.
DR   GO: GO:0003823; F:antigen binding; NAS.
DR   GO: GO:0006955; P:immune response; NAS.
DR   InterPro: IPR007110; IG-like.
DR   InterPro: IPR003596; IG_V.
DR   Pfam: PF00047; Ig_1.
DR   SMART, SM00406; IGV_1.
DR   PROSITE, PS00835; IG_LIKE, 1.
KW   Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DOMAIN          1      23      Framework-1.
FT   DOMAIN          24     34      Complementarity-determining-1.
FT   DOMAIN          35     49      Framework-2.
FT   DOMAIN          50     56      Complementarity-determining-2.
FT   DOMAIN          57     88      Framework-3.
FT   DOMAIN          89     97      Framework-4.
FT   DOMAIN          98    107      Complementarity-determining-3.
FT   DISULFID        23      88
FT   NON_TER         108     108
SQ   SEQUENCE      108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

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Query Match      80.7%; Score 464; DB 1; Length 108;
Best Local Similarity 81.5%; Pred. No. 5.5e-40;
Matches 88; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

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Qy      1 DIQLTQSPFSLASVGDRTITCRASQGISSTLANIYQKPKAPNLLIYASTLQSGVPS 60
      1 DIQLTQSPFSLASVGDRTITCRASQGISSTLANIYQKPKAPNLLIYASTLQSGVPS 60
Db      1 DIQLTQSPFSLASVGDRTITCRASQGISSTLANIYQKPKAPNLLIYASTLQSGVPS 60
Qy      61 RFGSGSGCTDFLTLLTISLQPEDFATYCCQYSTVPTFGQGTKEIKR 108
      61 RFGSGSGCTDFLTLLTISLQPEDFATYCCQYSTVPTFGQGTKEIKR 108
Db      61 RFGSGSGCTDFLTLLTISLQPEDFATYCCQYSTVPTFGQGTKEIKR 108

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Search completed: March 14, 2005, 20:49:19
Job time : 78.193 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 14, 2005, 20:21:17 ; Search time 94.4518 Seconds
(without alignments)
483.186 Million cell updates/sec

Title: US-09-723-752B-116

Perfect score: 658
Sequence: 1 EVQLVESGGGLVQPGSSLR.....YPRYTSTHMYFDVWGQRTL 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing filter 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1808:*
- 2: geneseqp1908:*
- 3: geneseqp2008:*
- 4: geneseqp2018:*
- 5: geneseqp2028:*
- 6: geneseqp2038:*
- 7: geneseqp2048:*
- 8: geneseqp2058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	658	100.0	118	2	AAW70686 Anti-VEGF
2	658	100.0	118	2	AAW70688 Anti-VEGF
3	658	100.0	118	3	AAAB1385 Anti-VEGF
4	658	100.0	118	3	AAAB1384 Anti-VEGF
5	658	100.0	118	5	ABP61255 Humanised
6	658	100.0	118	5	ABP61257 Humanised
7	658	100.0	123	8	ADG31769 V(H) doma
8	658	100.0	254	5	ABP51953 Plasmid p
9	658	100.0	476	5	ABP51953 Plasmid p
10	658	100.0	476	8	ADG14129 Plasmid p
11	658	100.0	476	8	ADG14129 Plasmid p
12	654	99.4	117	7	ADP09953 Antibody
13	654	99.4	117	7	ADP09953 Antibody
14	649	98.6	118	7	AAW70682 Anti-VEGF
15	649	98.6	118	3	AAAB05900 F(ab)-12
16	649	98.6	118	3	AAAB05900 F(ab)-12
17	649	98.6	118	5	ABP61251 Humanised
18	649	98.6	118	5	ABP61251 Humanised
19	640	97.3	118	2	AAW70684 Anti-VEGF
20	640	97.3	118	3	AAAB1383 Anti-VEGF
21	640	97.3	118	5	ABP61253 Humanised
22	640	97.3	121	8	ADG31894 V(H) prot
23	638	97.0	123	8	ADG31894 V(H) prot
24	635	96.5	118	2	AAW70678 Anti-VEGF
25	635	96.5	118	3	AAAB05899 Humanised

26	635	96.5	118	3	AAAB1381 F(ab)-12
27	635	96.5	118	3	AAAB1389 Anti-VEGF
28	635	96.5	118	5	ABP61247 Humanised
29	635	96.5	123	2	AAW70617 Anti-VEGF
30	635	96.5	123	5	ABP61186 Humanised
31	635	96.5	123	8	ADG31767 V(H) doma
32	635	96.5	123	8	ADG31780 V(H) doma
33	635	96.5	231	7	ADG26155 Parent an
34	635	96.5	231	7	ADG26155 Parent an
35	633	96.2	123	8	ADG31892 V(H) prot
36	631	95.9	118	2	AAW70680 Anti-VEGF
37	631	95.9	118	5	ABP61249 Humanised
38	629	95.6	123	5	ABP61266 Humanised
39	629	95.6	123	5	ABP61266 Humanised
40	627.5	95.4	121	3	AAAB05902 F(ab)-12
41	627.5	95.4	121	3	AAAB05902 F(ab)-12
42	627.5	95.4	121	3	AAAB1391 Anti-VEGF
43	625.5	95.1	234	7	ADG26161 Anti-VEGF
44	620.5	94.3	234	7	ADG26163 Anti-VEGF
45	618	93.9	123	2	AAW70626 Humanised

ALIGNMENTS

RESULT 1
AAW70686 standard; peptide; 118 AA.
XX
XX
AC AAW70686;
XX
XX
DT 27-JUN-1999 (first entry)
XX
XX
DE Anti-VEGF humanised antibody variable heavy domain of variant Y0313-1.
XX
XX Heavy variable domain; murine; humanised antibody;
XX anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
XX VEGF-induced angiogenesis; tumour; retinal disorder;
XX age-related macular degeneration; diabetic retinopathy;
XX rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX
XX Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
XX W09845331-A2.
XX
XX 15-OCT-1998.
XX
XX 03-APR-1998; 98MO-US006604.
XX
XX 07-APR-1997; 97US-00833504.
XX 06-AUG-1997; 97US-00908469.
XX
XX (GETH) GENENTECH INC.
XX
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
PI WPI; 1998-568337/48.
XX
XX New humanised antibody with affinity for vascular endothelial growth
XX factor - for treatment of tumours, retinal disease and other angiogenic
XX states, also related nucleic acid, vectors and transformed cells.
XX
XX Example 3; Fig 10B; 100pp; English.
XX
XX The present sequence represents a variable heavy domain of an affinity-
XX maturated anti-vascular endothelial growth factor (anti-VEGF) antibody
XX variant. The sequence is used in the course of the invention to produce
XX the humanised anti-VEGF antibody of the invention. The humanised
XX antibodies are used to inhibit VEGF-induced angiogenesis, particularly
XX for treating or preventing tumours (of any type) and retinal disorders
XX (e.g. age-related macular degeneration or diabetic retinopathy). They can

CC also be used to treat other conditions that involve angiogenesis, e.g.
 CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
 XX
 SQ Sequence 118 AA;

Query Match 100.0%; Score 658; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2,66-56;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWRQAPGKLEWVGINTYTGSEPT 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWRQAPGKLEWVGINTYTGSEPT 60
 QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYRYGTSHWYFDWGQGT 118
 DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYRYGTSHWYFDWGQGT 118

RESULT 2

AAW70688
 ID AAW70688 standard; peptide, 118 AA.

AC AAW70688;
 XX
 DT 27-JAN-1999 (first entry)
 DE Anti-VEGF humanised antibody variable heavy domain of variant Y0317.

KM Heavy variable domain; murine; humanised antibody;
 KM anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
 KM VEGF-induced angiogenesis; tumour; retinal disorder;
 KM age-related macular degeneration; diabetic retinopathy;
 KM rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.

XX WO9845331-A2.
 XX PD 15-OCT-1998.

XX PF 03-APR-1998; 98WO-US006604.
 XX PR 07-APR-1997; 97US-00833504.
 XX PR 06-AUG-1997; 97US-00908469.

XX PA (GETH) GENENTECH INC.

XX PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
 XX WPI; 1998-568337/48.

XX New humanised antibody with affinity for vascular endothelial growth
 PT factor - for treatment of tumours, retinal disease and other angiogenic
 PT states; also related nucleic acid, vectors and transformed cells.

XX Claim 25; Fig 10B; 100pp; English.

XX The present sequence represents a variable heavy domain of an affinity-
 CC matured anti-vascular endothelial growth factor (anti-VEGF) antibody
 CC variant. The sequence is used in the course of the invention to produce
 CC the humanised anti-VEGF antibody of the invention. The humanised
 CC antibodies are used to inhibit VEGF-induced angiogenesis, particularly
 CC for treating or preventing tumours (of any type) and retinal disorders
 CC (e.g. age-related macular degeneration or diabetic retinopathy). They can
 CC also be used to treat other conditions that involve angiogenesis, e.g.
 CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc

XX Sequence 118 AA;

Query Match 100.0%; Score 658; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2,66-56;

Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWRQAPGKLEWVGINTYTGSEPT 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWRQAPGKLEWVGINTYTGSEPT 60
 QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYRYGTSHWYFDWGQGT 118
 DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYRYGTSHWYFDWGQGT 118

RESULT 3

AA13385
 ID AA13385 standard; protein, 118 AA.

AC AA13385;
 XX
 DT 21-NOV-2000 (first entry)
 DE Anti-VEGF antibody Y0317 heavy chain variable domain.

KM Y0317; vascular endothelial cell growth factor; VEGF; antibody;
 KM antiinflammatory; cerebroprotective; cytostatic; antirheumatic;
 KM antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic;
 KM antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
 KM psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
 KM neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
 KM tissue transplantation; inflammation; oedema; trauma;
 KM complementarity determining region; CDR.

XX Unidentified.

XX Key Location/Qualifiers
 FH Region 26..35
 FT /label= CDR-H1
 FT 50..66
 FT /label= CDR-H2
 FT 70..79
 FT /label= CDR-7
 FT 99..112
 FT Region /label= CDR-H3

XX WO200037502-A2.

XX PD 29-JUN-2000.

XX PF 09-DEC-1999; 99WO-US029475.

XX PR 22-DEC-1998; 98US-00218481.

XX PA (GETH) GENENTECH INC.

XX PI Van Bruggen N, Ferrara N;

XX WPI; 2000-442646/38.

XX Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,
 PT diabetes and chronic inflammation in a mammal, comprises administering a
 PT human vascular endothelial cell growth factor antagonist.

XX Disclosure; Fig 14B; 60pp; English.

XX The present sequence is the heavy chain variable region of the affinity
 CC matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody
 CC Y0317. Humanised F(ab)-12 and affinity matured anti-VEGF antibodies may
 CC be used to treat conditions characterised by undesirable excessive
 CC neovascularisation. Such conditions include tumours (especially solid
 CC ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
 CC other retinopathies, retrolental fibroplasia, age-related macular
 CC degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias
 CC (including Grave's disease), corneal and other tissue transplantation,
 CC and chronic inflammation. Oedemas associated with tumours, strokes and
 CC head trauma, and aetiologies associated with malignancies, meigs' syndrome,

CC lung inflammation, nephrotic syndrome, pericardial effusion and pleural
CC effusion, may also be treated. Monoclonal antibodies are generated in
CC hybridoma cells and those with affinity for VEGF are identified by
CC immunoprecipitation or by an in vitro binding assay
XX

SO Sequence 118 AA:

Query Match 100.0%; Score 658; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.6e-56;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DQ 1 EVOLVESGGGLVOPGSLRLSCAASGYPFTHYGMMWRQAPGKLEWVGWINTYTGEPT 60
1 EVOLVESGGGLVOPGSLRLSCAASGYDFTHYGMWVRQAPGKLEWVGWINTYTGEPT 60
DB 61 AADPKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYVYGTSHWYFDWVGQGL 118
61 AADPKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYVYGTSHWYFDWVGQGL 118

RESULT 4
AAB13384
ID AAB13384 standard; protein; 118 AA.

AC AAB13384;
DT 21-NOV-2000 (first entry)

DE Anti-VEGF antibody Y0313-1 heavy chain variable domain.

KM Y0313-1; vascular endothelial cell growth factor; VEGF; antibody;
KM antiinflammatory; cerebroprotective; cyostatic; antirheumatic;
KM antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic;
KM antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
KM psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
KM neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
KM tissue transplantation; inflammation; oedema; trauma;
KM complementarity determining region; CDR.

OS Unidentified.

XX
FH Key Location/Qualifiers
FT Region /label= CDR-H1
FT Region /label= CDR-H2
FT Region /label= CDR-H3
FT Region /label= CDR-H3
FT Region /label= CDR-H3

MO200037502-A2.

29-JUN-2000.

09-DEC-1999; 99WO-US029475.

22-DEC-1998; 98US-00218481.

(GERTH) GENENTECH INC.

Van Bruggen N, Ferrara N;

WPI; 2000-442646/38.

PT Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,
PT diabetes and chronic inflammation in a mammal, comprises administering a
PT human vascular endothelial cell growth factor antagonist.
XX

PS Disclosure; Fig 14B; 60pp; English.

CC The present sequence is the heavy chain variable region of the affinity
CC matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody

CC Y0313-1. Humanised F(ab)-12 and affinity matured anti-VEGF antibodies may
CC be used to treat conditions characterised by undesirable excessive
CC neovascularisation. Such conditions include tumours (especially solid
CC ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
CC other retinopathies, retrolental fibroplasia, age-related macular
CC degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias
CC (including Grave's disease), corneal and other tissue transplantation,
CC and chronic inflammation. Oedemas associated with tumours, strokes and
CC head trauma, and ascites associated with malignancies, meigs' syndrome,
CC lung inflammation, nephrotic syndrome, pericardial effusion and pleural
CC effusion, may also be treated. Monoclonal antibodies are generated in
CC hybridoma cells and those with affinity for VEGF are identified by
CC immunoprecipitation or by an in vitro binding assay
XX

SO Sequence 118 AA:

Query Match 100.0%; Score 658; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.6e-56;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DQ 1 EVOLVESGGGLVOPGSLRLSCAASGYDFTHYGMWVRQAPGKLEWVGWINTYTGEPT 60
1 EVOLVESGGGLVOPGSLRLSCAASGYDFTHYGMWVRQAPGKLEWVGWINTYTGEPT 60
DB 61 AADPKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYVYGTSHWYFDWVGQGL 118
61 AADPKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYVYGTSHWYFDWVGQGL 118

RESULT 5
ABP61255
ID ABP61255 standard; protein; 118 AA.

AC ABP61255;
DT 20-SEP-2002 (first entry)

DE Humanised anti-VEGF Y0313-1 antibody variable heavy domain.

KM Cyostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
KM vascular endothelial growth factor; angiogenesis inhibitor; tumour;
KM retinal disorder; intracocular neovascular disorder; Y0313-1; heavy chain;
KM variable domain.

OS Homo sapiens.
OS Mus sp.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Domain /label= CDR-H1
FT Domain /label= CDR-H2
FT Domain /label= CDR-H3
FT Domain /label= CDR-H3
FT Domain /label= CDR-H3

US2002032315-A1.

14-MAR-2002.

06-APR-1998; 98US-00056160.

06-AUG-1997; 97US-0054856P.

PA (BACA/) BACA M.
PA (WELU/) WELUS J A.
PA (PREST/) PRESTA L G.
PA (LOWM/) LOWMAN H B.
PA (CHEN/) CHEN Y M.

PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI, 2002-517920/55.
 DR New humanised anti-VEGF (vascular endothelial growth factor) antibodies
 XX or their variants, useful for inhibiting VEGF-induced angiogenesis in a
 PT mammal, particularly for treating tumor or retinal disorders.
 XX Example 3; Fig 10; 47pp; English.
 PS
 CC The present invention relates to humanised anti-VEGF (vascular
 CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
 CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
 CC particularly those having a tumor or a retinal disorder e.g. intracocular
 CC neovascular disorders. The present sequence is an exemplary heavy chain
 CC variable domain of the humanised anti-VEGF antibody of the invention
 XX
 SQ Sequence 118 AA;
 Query Match 100.0%; Score 658; DB 5; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2.6e-56;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTTGEPT 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTTGEPT 60
 Oy 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYYYGTSHWYFDVWGQGT 118
 Db 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYYYGTSHWYFDVWGQGT 118

RESULT 6
 ABP61257
 ID ABP61257 standard; protein; 118 AA.
 AC ABP61257;
 XX
 DT 20-SEP-2002 (first entry)
 XX
 DB Humanised anti-VEGF Y0317 antibody variable heavy domain.
 XX
 KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
 KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
 KW retinal disorder; intracocular neovascular disorder; Y0317; heavy chain;
 KW variable domain.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Domain 26..35
 FT Domain /label= CDR-H1
 FT Domain 50..66
 FT Domain /label= CDR-H2
 FT Domain 70..79
 FT Domain /label= CDR-7
 FT Domain 99..112
 FT Domain /label= CDR-H3
 XX
 PN US2002032315-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 06-APR-1998; 98US-00056160.
 XX
 PR 06-AUG-1997; 97US-0054856P.
 XX
 PA (BACA/) BACA M.
 PA (WELL/) WELLS J A.
 PA (PRES/) PRESTA L G.
 PA (LOWM/) LOWMAN H B.

PA (CHEN/) CHEN Y M.
 XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
 PI WPI, 2002-517920/55.
 DR
 XX
 PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
 PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
 PT mammal, particularly for treating tumor or retinal disorders.
 XX
 PS Claim 25; Fig 10; 47pp; English.
 CC The present invention relates to humanised anti-VEGF (vascular
 CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
 CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
 CC particularly those having a tumor or a retinal disorder e.g. intracocular
 CC neovascular disorders. The present sequence is an exemplary heavy chain
 CC variable domain of the humanised anti-VEGF antibody of the invention
 XX
 SQ Sequence 118 AA;
 Query Match 100.0%; Score 658; DB 5; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2.6e-56;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTTGEPT 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTTGEPT 60
 Oy 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYYYGTSHWYFDVWGQGT 118
 Db 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYYYGTSHWYFDVWGQGT 118

RESULT 7
 ADG31769
 ID ADG31769 standard; protein; 123 AA.
 AC ADG31769;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DB V(H) domain of matured humanised murine anti-VEGF antibody SeqID3.
 XX
 KW protein library; in silico; VEGF; vascular endothelial growth factor;
 KW antibody; computational prediction; V(H) domain; mouse; murine.
 XX
 OS Synthetic.
 OS Mus sp.
 OS
 PN WO2003099999-A2.
 XX
 PD 04-DEC-2003.
 XX
 PF 20-MAY-2003; 2003WO-US016037.
 XX
 PR 20-MAY-2002; 2002US-00153159.
 PR 20-MAY-2002; 2002US-00153176.
 XX
 PA (ABMA-) ABMAXIS INC.
 XX
 PI Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S;
 XX WPI, 2004-035117/03.
 DR
 XX
 PT Constructing antibody libraries for generating protein libraries with
 PT improved biological function comprising selecting from tester protein
 PT sequences two peptide segments having 15 sequence identity with the lead
 PT sequence.
 XX
 PS Disclosure; SEQ ID NO 3; 354pp; English.
 XX

CC This invention relates to a novel method for the generation and screening
CC of a protein library in *silico*. Specifically, it refers to a high-
CC throughput method optimised for the identification of anti-VEGF (vascular
CC endothelial growth factor) antibodies with improved binding affinities
CC for their target antigen (VEGF), using computational prediction. The
CC present invention describes selecting proteins with a desirable function
CC based on their structural similarity to the target structural or
CC functional motif of a lead protein of interest. Accordingly, these
CC protein libraries are functionally biased with increased diversity so as
CC to increase the chance of identifying novel hits or combinations of
CC mutants with enhanced binding affinity. Furthermore, the sequence profile
CC based on the multiple structure alignment of the available lead structure
CC allows the sampling of a larger sequence space than by traditional,
CC multiple sequence alignment approaches. This polypeptide sequence is the
CC V(H) domain of affinity matured humanised murine anti-VEGF antibody, used
CC in an exemplification of the invention.

CC Sequence 123 AA;

Query Match 100.0%; Score 658; DB 8; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.7e-56;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMNVRQAPGKLEWVGWINTYGEPT 60
1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMNVRQAPGKLEWVGWINTYGEPT 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMNVRQAPGKLEWVGWINTYGEPT 60
Qy 61 AADFKRRFTPSLDTSKSTAYVLQMSLRABEDTAVYCAKPYPGYGTSHWYFDWGQSTL 118
61 AADFKRRFTPSLDTSKSTAYVLQMSLRABEDTAVYCAKPYPGYGTSHWYFDWGQSTL 118
Db 61 AADFKRRFTPSLDTSKSTAYVLQMSLRABEDTAVYCAKPYPGYGTSHWYFDWGQSTL 118

RESULT 8
ABP51953
ID ABP51953 standard; protein; 254 AA.

XX ABP51953;
XX
DT 09-OCT-2002 (first entry)

XX Plasmid pY0317 anti-VEGF Fab amino acid sequence SEQ ID NO:2 #2.

XX Bacterial host; protease; degP; prc; apr; anti-VEGF antibody; antibody;
XX humanised; Apo2 ligand; anti-CD18; anti-tissue factor; 2C4; anti-CD20;
XX anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;
XX anti-CD11a; Fab'; Fab'2; Fab'2-leucine zipper fusion; anti-VEGF Fab.

OS Mus sp.
OS Escherichia coli.
OS Synthetic.

XX Key Location/Qualifiers
XX Peptide 1..23
XX /label= signal
XX Protein 24..254
XX /label= anti-VEGF_Fab

XX WO200248376-A2.

XX 20-JUN-2002.

XX 07-DEC-2001; 2001WO-US047581.

XX 14-DEC-2000; 2000US-0256162P.

XX (GETH) GENENTECH INC.

XX Chen CY;

XX WPI, 2002-583522/62.

XX DR N-PSDB; ABQ73919.

XX Novel Escherichia coli strain useful for producing polypeptide, deficient

PT in degP and prc encoding protease, and harboring mutant apr gene, product
PT of gene suppresses growth phenotypes of strains harboring prc mutants.

XX Example 1; Fig 1D-E; 63pp; English.

XX The present invention describes an Escherichia coli strain (1) deficient
XX in chromosomal degP and prc gene, the product of mutant apr gene
XX and harbouring a mutant apr gene, the product of mutant prc gene
XX suppresses growth phenotypes exhibited by strains harbouring prc mutants.
XX (1) is useful for producing a polypeptide, by culturing (1) comprising
XX nucleic acid encoding the polypeptide, which is heterologous to the
XX strain, such that the nucleic acid is expressed, and recovering the
XX heterologous polypeptide from the strain. The heterologous polypeptide is
XX proteolytically sensitive. Culturing of (1) is performed in a fermentor
XX under conditions of high- or low-cell density fermentation. The
XX polypeptide is recovered from the periplasm or culture medium of the
XX strain. The polypeptide is an antibody (humanised or full-length
XX antibody) or Apo2 ligand. The antibody is an anti-CD18, anti-vascular
XX endothelial growth factor (VEGF), anti-tissue factor, 2C4, anti-Her-2,
XX anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an
XX antibody fragment having a light chain (kappa light chain). The antibody
XX fragment is a Fab, Fab', Fab'2 or Fab'2-leucine zipper fusion, anti-CD18
XX Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper
XX fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-
XX tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, or anti-
XX CD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18
XX Fab'2-leucine zipper fusion with a 6-lysine tag. The present sequence
XX represents an anti-VEGF Fab amino acid sequence from the present
XX invention

XX Sequence 254 AA;

Query Match 100.0%; Score 658; DB 5; Length 254;
Best Local Similarity 100.0%; Pred. No. 6.1e-56;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMNVRQAPGKLEWVGWINTYGEPT 60
24 EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMNVRQAPGKLEWVGWINTYGEPT 83
Db 24 EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMNVRQAPGKLEWVGWINTYGEPT 83

Qy 61 AADFKRRFTPSLDTSKSTAYVLQMSLRABEDTAVYCAKPYPGYGTSHWYFDWGQSTL 118
64 AADFKRRFTPSLDTSKSTAYVLQMSLRABEDTAVYCAKPYPGYGTSHWYFDWGQSTL 141
Db 64 AADFKRRFTPSLDTSKSTAYVLQMSLRABEDTAVYCAKPYPGYGTSHWYFDWGQSTL 141

RESULT 9
ABB81110
ID ABB81110 standard; protein; 476 AA.

XX ABB81110;
XX

XX 05-NOV-2002 (first entry)

XX Anti-VEGF heavy chain fragment.

XX Immunoglobulin; promoter; cytosolic; antiinflammatory; immunomodulator;
XX neuroprotective; CD11; tissue factor; vascular endothelial growth factor;
XX VEGF.

XX Synthetic.

XX Key Location/Qualifiers
XX Peptide 1..23
XX /note= "STII signal sequence TR-1"
XX Protein 24..476
XX /note= "anti-VEGF heavy chain"

XX WO200261090-A2.

XX 08-AUG-2002.

XX 13-DEC-2001; 2001WO-US048691.

XX

PR 14-DEC-2000; 2000US-0256164P.
 XX (GETH) GENENTECH INC.
 PA
 XX
 PI Simons LC, Kilmowski L, Reilly DE, Yaneura DG;
 XX
 DR MPI: 2002-619253/66.
 XX N-PESDB; ABR86646.
 DR
 XX New polynucleotide comprising first and second promoter-cistron pairs,
 PT useful for diagnosing, treating or preventing diseases associated with
 PT abnormal expression and/or activity of antigens such as inflammatory
 PT disorders.
 XX
 PS Disclosure; Fig 21A-C; 104pp; English.
 XX
 CC The invention provides a polynucleotide, which encodes an immunoglobulin
 CC (Ig), comprising a first or second promoter-cistron pair consisting of a
 CC first or second promoter and cistron, respectively. The first cistron of
 CC the first promoter-cistron pair comprises a first translational
 CC initiation region (TIR-L) operably linked to a nucleic acid sequence
 CC encoding an Ig light chain and the second cistron of the second promoter-
 CC cistron pair comprises a second translational initiation region (TIR-H)
 CC operably linked to a nucleic acid sequence encoding an Ig heavy chain.
 CC Upon expression of the polynucleotide in a prokaryotic host cell, light
 CC and heavy chains are folded and assembled to form a biologically active
 CC Ig. The antibody of the invention is useful for diagnosing, treating or
 CC preventing diseases or conditions associated with abnormal expression and
 CC /or activity of one or more antigen molecules e.g. lymphoid malignancies,
 CC inflammatory, angiogenic, immunologic, neuronal, glial, astrocytic,
 CC hypothalamic or other glandular disorders. The present sequence
 CC represents the amino acid sequence of an anti-vascular endothelial growth
 CC factor (VEGF) heavy chain fragment of the cistron vector pXVG2AP11
 CC
 SQ Sequence 476 AA;
 XX
 Query Match 100.0%; Score 658; DB 5; Length 476;
 Best Local Similarity 100.0%; Pred. No. 1.2e-55;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVOLVESGGGLVOPGSLRLSCAASGYDFTHYGMNWVROAPGKLEWGMINTYGEPT 60
 DB 24 EVQLVESGGGLVOPGSLRLSCAASGYDFTHYGMNWVROAPGKLEWGMINTYGEPT 83
 QY 61 AADFRKRFPSIDTSKSTAYLQMSLRADPTAVYCAKPYGYGSHWYFDWGQGT 118
 DB 84 AADFRKRFPSIDTSKSTAYLQMSLRADPTAVYCAKPYGYGSHWYFDWGQGT 141
 RESULT 10
 ID ADO14129 standard; protein; 476 AA.
 XX
 AC ADO14129;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Plasmid pXVG2AP11 expression cassette heavy chain protein SEQ ID NO:9.
 XX
 KW antibody; variant heavy chain hinge region; immunoconjugate; cytostatic;
 KW immunosuppressive; immunotherapy; tumour; cancer; immune disorder;
 KW expression cassette; plasmid pXVG2AP11; anti-VEGF heavy chain.
 XX
 OS Synthetic.
 XX
 PN WO2004042017-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 30-OCT-2003; 2003WO-US034610.
 XX
 PR 31-OCT-2002; 2002US-0422952P.
 XX

PA (GETH) GENENTECH INC.
 XX
 XX Reilly D, Yaneura DG;
 XX
 DR MPI: 2004-390607/36.
 XX N-PESDB; ADO14127.
 DR
 XX New antibody comprising a variant heavy chain hinge region incapable of
 PT inter-heavy chain disulfide linkage, useful for treating, preventing,
 PT diagnosing, delaying or preventing a disease, e.g. tumor, cancer or
 PT immune disorder.
 XX
 PS Example 1; SEQ ID NO 9; 124pp; English.
 XX
 CC The present invention describes an antibody comprising a variant heavy
 CC chain hinge region incapable of inter-heavy chain disulfide linkage. Also
 CC described: (1) an antibody lacking inter-heavy chain disulfide linkage;
 CC (2) an immunoconjugate comprising the antibody conjugated with a
 CC heterologous moiety; (3) a composition comprising the antibody or
 CC immunoconjugate, and carrier; (4) an article of manufacture comprising
 CC the composition in a container; (5) a polynucleotide encoding the
 CC antibody or immunoconjugate, or a variant immunoglobulin heavy chain
 CC incapable of inter-heavy chain disulfide linkage; (6) a recombinant
 CC vector for expressing the antibody or immunoconjugate; (7) a host cell
 CC comprising the recombinant vector; (8) expressing in a host cell an
 CC antibody or interest in which at least one inter-heavy chain disulfide
 CC linkage is eliminated, and recovering the antibody from the host cell;
 CC (9) an aglycosylated antibody produced by the method; and (10) treating,
 CC preventing, diagnosing, delaying or preventing a disease in a subject.
 CC The antibody has cytostatic and immunosuppressive activities, and can be
 CC used in immunotherapy. The antibody, immunoconjugate and methods are
 CC useful for treating, preventing, diagnosing, delaying or preventing a
 CC disease, e.g. tumour, cancer or immune disorder. The present sequence
 CC represents the anti-VEGF heavy chain from the expression cassette of
 CC plasmid pXVG2AP11, which is used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 476 AA;
 XX
 Query Match 100.0%; Score 658; DB 8; Length 476;
 Best Local Similarity 100.0%; Pred. No. 1.2e-55;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVOLVESGGGLVOPGSLRLSCAASGYDFTHYGMNWVROAPGKLEWGMINTYGEPT 60
 DB 24 EVQLVESGGGLVOPGSLRLSCAASGYDFTHYGMNWVROAPGKLEWGMINTYGEPT 83
 QY 61 AADFRKRFPSIDTSKSTAYLQMSLRADPTAVYCAKPYGYGSHWYFDWGQGT 118
 DB 84 AADFRKRFPSIDTSKSTAYLQMSLRADPTAVYCAKPYGYGSHWYFDWGQGT 141
 RESULT 11
 ID ADO90730 standard; protein; 476 AA.
 XX
 AC ADO90730;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Anti-VEGF antibody Y0317 heavy chain protein SEQ ID NO:7.
 XX
 KW antibody; antigen binding fragment; cell culture; variable domain;
 KW modified framework region; hypervariable region; cytostatic;
 KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; heavy chain.
 XX
 OS Homo sapiens.
 XX
 OS Synthetic.
 XX
 PN WO2004065417-A2.

XX 03-MAR-2003; 2003WO-US006598.
PF
XX
XX 01-MAR-2002; 2002US-0360843P.
PR
XX 29-MAY-2002; 2002US-0384197P.
PR
XX
PA (XENC-) XENCOR.
XX
PI Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B,
XX
XX WPI; 2003-722066/68.
XX
XX Computer optimization of physicochemical properties of antibodies
PT comprises analyzing the interactions of amino acids at variable
XX positions.
XX
XX Example 6; Fig 16a; 135pp; English.
XX
XX The present invention relates to a method for optimizing at least one
CC physico-chemical property of an antibody by a computational screening
CC method. The method comprises: receiving a template antibody structure;
CC selecting at least one variable position belonging to the antibody
CC structure; selecting at least one amino acid to be considered at the
CC variable position(s); analyzing the interaction of each selected amino
CC acid at each variable position with at least part of the remainder of the
CC antibody, including the selected amino acids at other variable positions;
CC and identifying a set of at least one antibody sequence with at least one
CC optimized physico-chemical property. The method is useful for stabilizing
CC the physico-chemical properties of an antibody, especially the stability,
CC solubility, or antigen binding affinity. The optimized antibody may be
CC useful for treating a patient. The present sequence is an antibody
CC variable region sequence used to illustrate the invention.
XX
XX Sequence 117 AA;
SQ
Query Match 99.4%; Score 654; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.3e-56;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMMWRQAPGKLEWVGINTYGEPT 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMMWRQAPGKLEWVGINTYGEPT 60
QY 61 AADPKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYRYGSHYFPDWGGCT 117
DB 61 AADPKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYRYGSHYFPDWGGCT 117
RESULT 14
AAW70682
ID AAW70682 standard; peptide; 118 AA.
XX
XX AAW70682;
AC
XX
XX 27-JAN-1999 (first entry)
DT
XX
XX Anti-VEGF humanised antibody variable heavy domain of variant Y0243-1.
DB
XX
XX Heavy variable domain; murine; humanised antibody;
XX anti-vascular endothelial growth factor antibody;
XX VEGF-induced angiogenesis; tumour; retinal disorder;
XX age-related macular degeneration; diabetic retinopathy;
XX rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX
XX Synthetic.
OS
XX Mue sp.
OS
XX Homo sapiens.
OS
XX MO3845331-A2.
PN
XX
XX 15-OCT-1998.
PD
XX
XX 03-APR-1998; 98WO-US006604.
PF

XX 07-APR-1997; 97US-00833504.
PR
XX 06-AUG-1997; 97US-00908469.
PR
XX
XX (GETH) GENENTECH INC.
XX
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM,
XX
XX WPI; 1998-56837/48.
XX
XX New humanised antibody with affinity for vascular endothelial growth
PT factor - for treatment of tumours, retinal disease and other angiogenic
PT states, also related nucleic acid, vectors and transformed cells.
XX
XX Example 3; Fig 10B; 100pp; English.
XX
XX The present sequence represents a variable heavy domain of an affinity-
CC matured anti-vascular endothelial growth factor (anti-VEGF) antibody
CC variant. The sequence is used in the course of the invention to produce
CC the humanised anti-VEGF antibody of the invention. The humanised
CC antibodies are used to inhibit VEGF-induced angiogenesis, particularly
CC for treating or preventing tumours (of any type) and retinal disorders.
CC (e.g. age-related macular degeneration or diabetic retinopathy). They can
CC also be used to treat other conditions that involve angiogenesis, e.g.
CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
XX
XX Sequence 118 AA;
SQ
Query Match 98.6%; Score 649; DB 2; Length 118;
Best Local Similarity 98.3%; Pred. No. 2e-55;
Matches 116; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMMWRQAPGKLEWVGINTYGEPT 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMMWRQAPGKLEWVGINTYGEPT 60
QY 61 AADPKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYRYGSHYFPDWGGCT 118
DB 61 AADPKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYRYGSHYFPDWGGCT 118
RESULT 15
AAB05900
ID AAB05900 standard; peptide; 118 AA.
XX
XX AAB05900;
AC
XX
XX 17-OCT-2000 (first entry)
DT
XX
XX F(ab)-12 antibody variant Y0238-3 heavy chain variable domain.
DB
XX
XX Humanised, F(ab)-12, heavy chain variable domain; antibody variant;
XX phage display; randomised library; cytotoxic; antiarteriosclerotic;
XX antiapoptotic; antidiabetic; antiinflammatory; antiarteriosclerotic;
XX vascular endothelial growth factor; VEGF; breast cancer; lung cancer;
XX retinoblastoma; rheumatoid arthritis; psoriasis; atherosclerosis;
XX diabetic retinopathy; complementarity determining region; CDR.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX MO200029584-A1.
PN
XX
XX 25-MAY-2000.
PD
XX
XX 16-NOV-1999; 99WO-US027153.
PF
XX
XX 18-NOV-1998; 98US-0108945P.
PR
XX
XX (GETH) GENENTECH INC.
PA
XX
XX Chen YM, Lowman HB, Muller Y,
XX
XX

DR MPI: 2000-387797/33.

XX Antibody variants with higher binding affinity than native antibodies
PT useful for diagnosis, prevention and treatment of neoplastic and non-
PT neoplastic diseases comprises amino acid insertion in hypervariable
PT region.

XX Disclousure: Fig 1B; 110pp; English.

XX The present sequence is the heavy chain variable domain of the F(ab)-12
CC antibody variant Y0238-3. F(ab)-12 is a humanised anti-vascular
CC endothelial growth factor (VEGF) antibody. F(ab)-12 was the parent
CC antibody used in the production of a large number of antibody variants
CC containing randomised peptide inserts within the complementarity
CC determining regions (CDRs). Phage display libraries were subjected to
CC eight rounds of selection to isolate variants with an antigen binding
CC affinity at least two-fold stronger than the binding affinity of parent
CC antibody for the target VEGF antibody. The anti-VEGF antibody variants
CC may be useful in diagnostic assays for detecting expression of VEGF in
CC cells, tissue or serum. They may also be used in the prevention and
CC treatment of neoplastic diseases such as breast cancer, lung cancer and
CC retinoblastoma, and non-neoplastic diseases including rheumatoid
CC arthritis, psoriasis, atherosclerosis, and diabetic and other
CC proliferative retinopathies

XX Sequence 118 AA:

Query Match 98.6%; Score 649; DB 3; Length 118;

Best Local Similarity 98.3%; Pred. No. 2e-55;

Matches 116; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 EVOIVESGGGLVOPGSLRLSCAAGYDPTHGGMWRQAPGKLEWGMINTYGEPT 60
   |||||
DB 1 EVQLVESGGGLVQPGSLRLSCAAGYDPTHGGMWRQAPGKLEWGMINTYGEPT 60
   |||||

QY 61 AADFRRRTFSLDTSKSTAYLQMSLRADTAIVYCAKYPYYGTSHWYFDVMGGTL 118
   |||||
DB 61 AADFRRRTFSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVMGGTL 118
   |||||
```

Search completed: March 14, 2005, 20:39:17
Job time : 95.4518 secs

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OM protein - protein search, using BW model

Run on: March 14, 2005, 20:30:13 ; Search time 24.3246 Seconds
(without alignments)
362.127 Million cell updates/sec

Title: US-09-723-752B-116

Perfect score: 658
Sequence: 1 EVOLVESGGGGLVOPGSGRLR.....YPIYGTSHWYFDWGQSTL 118

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	649	98.6	118 4 US-09-440-781-97	Sequence 97, Appl
2	635	96.5	118 4 US-09-440-781-96	Sequence 96, Appl
3	627.5	95.4	121 4 US-09-440-781-99	Sequence 99, Appl
4	613.5	93.2	121 4 US-09-440-781-98	Sequence 98, Appl
5	611	92.9	491 4 US-10-011-125A-2	Sequence 2, Appl1
6	507.5	77.1	118 1 US-08-425-336-126	Sequence 126, App
7	507.5	77.1	118 1 US-08-488-113B-126	Sequence 126, App
8	507.5	77.1	118 1 US-08-477-484B-126	Sequence 126, App
9	507.5	77.1	118 2 US-08-646-360-126	Sequence 126, App
10	507.5	77.1	118 3 US-08-839-765-126	Sequence 126, App
11	507.5	77.1	118 3 US-09-136-389-126	Sequence 126, App
12	507.5	77.1	118 3 US-09-610-838-126	Sequence 126, App
13	507.5	77.1	118 3 US-09-711-485-126	Sequence 126, App
14	507.5	77.1	240 1 US-08-488-113B-147	Sequence 147, App
15	507.5	77.1	240 1 US-08-488-113B-148	Sequence 148, App
16	507.5	77.1	240 1 US-08-477-484B-147	Sequence 147, App
17	507.5	77.1	240 1 US-08-477-484B-148	Sequence 148, App
18	507.5	77.1	240 2 US-08-646-360-147	Sequence 147, App
19	507.5	77.1	240 2 US-08-646-360-148	Sequence 148, App
20	507.5	77.1	240 3 US-08-839-765-147	Sequence 147, App
21	507.5	77.1	240 3 US-08-839-765-148	Sequence 148, App
22	507.5	77.1	240 3 US-09-136-389-147	Sequence 147, App
23	507.5	77.1	240 3 US-09-136-389-148	Sequence 148, App
24	507.5	77.1	240 3 US-09-610-838-147	Sequence 147, App
25	507.5	77.1	240 3 US-09-610-838-148	Sequence 148, App
26	507.5	77.1	240 4 US-09-711-485-147	Sequence 147, App
27	507.5	77.1	240 4 US-09-711-485-148	Sequence 148, App

28	493.5	75.0	118 1 US-08-107-669D-29	Sequence 29, Appl
29	493.5	75.0	118 1 US-08-472-788A-29	Sequence 29, Appl
30	493.5	75.0	118 2 US-08-477-531B-29	Sequence 29, Appl
31	493.5	75.0	118 2 US-08-062-842A-29	Sequence 29, Appl
32	492.5	74.8	118 1 US-08-107-669D-67	Sequence 67, Appl
33	492.5	74.8	118 1 US-08-472-788A-89	Sequence 89, Appl
34	492.5	74.8	118 2 US-08-477-531B-67	Sequence 67, Appl
35	492.5	74.8	118 2 US-08-062-842A-89	Sequence 89, Appl
36	491.5	74.7	122 2 US-07-934-373C-20	Sequence 20, Appl
37	491.5	74.7	122 3 US-08-437-642B-20	Sequence 20, Appl
38	491.5	74.7	122 4 US-08-146-206C-20	Sequence 20, Appl
39	491.5	74.7	122 4 US-09-705-686C-20	Sequence 20, Appl
40	491.5	74.7	122 4 US-09-705-392A-20	Sequence 20, Appl
41	491.5	74.7	122 4 US-09-705-392A-20	Sequence 20, Appl
42	491.5	74.7	122 5 PCT-US93-07832-20	Sequence 20, Appl
43	490.5	74.5	122 2 US-07-934-373C-45	Sequence 45, Appl
44	490.5	74.5	122 3 US-08-437-642B-45	Sequence 45, Appl
45	490.5	74.5	122 4 US-08-146-206C-26	Sequence 26, Appl

ALIGNMENTS

```
RESULT 1
US-09-440-781-97
Sequence 97, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yeet Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P146981
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 97
LENGTH: 118
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-118
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-97

Query Match      98.6%; Score 649; DB 4; Length 118;
Best Local Similarity 98.3%; Pred. No. 7.8e-59;
Matches 116; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVOLVESGGGGLVOPGSGRLRSCAAGYDFTYGNMWRQARQKGLWYGMINTYTGEPY 60
        |||
DB      1 EVOLVESGGGGLVOPGSGRLRSCAAGYDFTYGNMWRQARQKGLWYGMINTYTGEPY 60
        |||

QY      61 AADKRRPTFSLDPSKSTAYLQNMNSLRADTAIVYCAKYPYIYGTSHWYFDWGQSTL 118
        |||
DB      61 AADKRRPTFSLDPSKSTAYLQNMNSLRADTAIVYCAKYPYIYGTSHWYFDWGQSTL 118
        |||

RESULT 2
US-09-440-781-96
Sequence 96, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yeet Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P146981
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 96
LENGTH: 118
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
```

NAME/KEY: artificial
LOCATION: 1-118
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-96

Query Match 96.5%; Score 635; DB 4; Length 118;
Best Local Similarity 96.6%; Pred. No. 2, 1e-57;
Matches 114; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYPFTYGMNWVROAPGKLEWGMINTYGEPTY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYFTNYGMNWVROAPGKLEWGMINTYGEPTY 60
QY 61 AADFRKRPFTSLDTSKSTAYLQNNSLRAEDTAVYCAKYPYY--GTSHYFDVWGQGT 118
DB 61 AADFRKRPFTSLDTSKSTAYLQNNSLRAEDTAVYCAKYPHYGSSHWYFDVWGQGT 118

RESULT 3

US-09-440-781-99
Sequence 99, Application US/09440781
Patent No. 6632926

GENERAL INFORMATION:
APPLICANT: Yvonne Man-Yee Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99

SEQ ID NO 99
LENGTH: 121
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-121
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-99

Query Match 95.4%; Score 627.5; DB 4; Length 121;
Best Local Similarity 95.0%; Pred. No. 1, 3e-56;
Matches 115; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKLEWGMINTYGEPTY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKLEWGMINTYGEPTY 60
QY 61 AADFRKRPFTSLDTSKSTAYLQNNSLRAEDTAVYCAKYPYY--GTSHYFDVWGQGT 117
DB 61 AADFRKRPFTSLDTSKSTAYLQNNSLRAEDTAVYCAKYPHYVNERKSHWYFDVWGQGT 120

QY 118 L 118
DB 121 L 121

RESULT 4

US-09-440-781-98
Sequence 98, Application US/09440781
Patent No. 6632926

GENERAL INFORMATION:
APPLICANT: Yvonne Man-Yee Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99

SEQ ID NO 98
LENGTH: 121
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial

LOCATION: 1-121
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-98

Query Match 93.2%; Score 613.5; DB 4; Length 121;
Best Local Similarity 93.4%; Pred. No. 3, 4e-55;
Matches 113; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKLEWGMINTYGEPTY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYFTNYGMNWVROAPGKLEWGMINTYGEPTY 60
QY 61 AADFRKRPFTSLDTSKSTAYLQNNSLRAEDTAVYCAKYPYY--GTSHYFDVWGQGT 117
DB 61 AADFRKRPFTSLDTSKSTAYLQNNSLRAEDTAVYCAKYPHYVNERKSHWYFDVWGQGT 120

QY 118 L 118
DB 121 L 121

RESULT 5

US-10-011-125A-2
Sequence 2, Application US/1001125A
Patent No. 6828121

GENERAL INFORMATION:
APPLICANT: Chen, Christina Yu-Ching
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1804R1
CURRENT APPLICATION NUMBER: US/10/011,125A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 12

SEQ ID NO 2
LENGTH: 491
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized.
US-10-011-125A-2

Query Match 92.9%; Score 611; DB 4; Length 491;
Best Local Similarity 91.5%; Pred. No. 3, 2e-54;
Matches 108; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKLEWGMINTYGEPTY 60
DB 261 EVQLVESGGGLVQPGGSLRLSCAASGYFTNYGMNWVROAPGKLEWGMINTYGEPTY 320
QY 61 AADFRKRPFTSLDTSKSTAYLQNNSLRAEDTAVYCAKYPYYGTSHWYFDVWGQGT 118
DB 321 AADFRKRPFTSLDTSKSTAYLQNNSLRAEDTAVYCAKYPHYGSSHWYFDVWGQGT 378

RESULT 6

US-08-425-336-126
Sequence 126, Application US/08425336
Patent No. 5621083

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studlika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-425-336-126

Query Match 77.1%; Score 507.5; DB 1; Length 118;
Best Local Similarity 77.8%; Pred. No. 2.1e-44;
Matches 91; Conservative 12; Mismatches 9; Indels 5; Gaps 1;
QY 1 EVLVESGGGLVPGGSLRLSCAASGYDFTHYGMNVRQAPGKLEWGMINTYTGPTY 60
DB 1 EILVQSGGGLVPGGSLRLSCAASGYDFTHYGMNVRQAPGKLEWGMINTYTGPTY 60
QY 61 AADFKRFTFSLDTSKSTAYLQWNSLRADTAAYVCAKPYVYGTSHWYFDWVGQGT 117
DB 61 ADFKRFTEFLDTSKSTAYLQWNSLRADTAAYVCAKPYVYGTSHWYFDWVGQGT 112

RESULT 7
US-08-488-113B-126
Sequence 126, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B

FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Micholias, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-126

Query Match 77.1%; Score 507.5; DB 1; Length 118;
Best Local Similarity 77.8%; Pred. No. 2.1e-44;
Matches 91; Conservative 12; Mismatches 9; Indels 5; Gaps 1;
QY 1 EVLVESGGGLVPGGSLRLSCAASGYDFTHYGMNVRQAPGKLEWGMINTYTGPTY 60
DB 1 EILVQSGGGLVPGGSLRLSCAASGYDFTHYGMNVRQAPGKLEWGMINTYTGPTY 60
QY 61 AADFKRFTFSLDTSKSTAYLQWNSLRADTAAYVCAKPYVYGTSHWYFDWVGQGT 117
DB 61 ADFKRFTEFLDTSKSTAYLQWNSLRADTAAYVCAKPYVYGTSHWYFDWVGQGT 112

RESULT 8
US-08-477-484B-126
Sequence 126, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-126

Query Match 77.1%; Score 507.5; DB 1; Length 118;
Best Local Similarity 77.8%; Pred. No. 2.1e-44;
Matches 91; Conservative 12; Mismatches 9; Indels 5; Gaps 1;

QY 1 EVLVSSGGGLVPGGSLRLSQAAGYDFTYGMNWRQAPGKLEWVGINTYTGSEPTY 60
DB 1 EIQLVSSGGGLVPGGSLRLSQAAGYDFTYGMNWRQAPGKLEWVGINTYTGSEPTY 60
QY 61 AADPKRFTSLDTSKSTAYLQNNSLRAEDTAVYYCAKYPYYGTSHMYPDVWGQT 117
DB 61 AADPKRFTSLDTSKSTAYLQNNSLRAEDTAVYYCAKYPYYGTSHMYPDVWGQT 112

RESULT 9

US-08-646-360-126
Sequence 126, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studulka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-126

Query Match 77.1%; Score 507.5; DB 2; Length 118;
Best Local Similarity 77.8%; Pred. No. 2.1e-44;
Matches 91; Conservative 12; Mismatches 9; Indels 5; Gaps 1;

QY 1 EVLVSSGGGLVPGGSLRLSQAAGYDFTYGMNWRQAPGKLEWVGINTYTGSEPTY 60
DB 1 EIQLVSSGGGLVPGGSLRLSQAAGYDFTYGMNWRQAPGKLEWVGINTYTGSEPTY 60
QY 61 AADPKRFTSLDTSKSTAYLQNNSLRAEDTAVYYCAKYPYYGTSHMYPDVWGQT 117
DB 61 AADPKRFTSLDTSKSTAYLQNNSLRAEDTAVYYCAKYPYYGTSHMYPDVWGQT 112

RESULT 10

US-08-839-765-126
Sequence 126, Application US/08839765
Patent No. 614631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studulka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-839-765-126

Query Match 77.1%; Score 507.5; DB 3; Length 118;
Best Local Similarity 77.8%; Pred. No. 2.1e-44;
Matches 91; Conservative 12; Mismatches 9; Indels 5; Gaps 1;
QY 1 EVOLVSGGGLVOPGSLRLSCAASGYDFTHYGMNVVROAPGKLEWVGINTYGEPT 60
DB 1 EIQLVSGGGLVPGGSVRLSCAASGYFTTNGMNVVROAPGKLEWVGINTHTEPT 60
QY 61 AADFKRFTFSLDTSKSTAYLQNSLRADTAAYVYCAKYPYVYGTSHWYFDVWGQT 117
DB 61 ADFKRFRTFSLDTSKSTAYLQNSLRADTAAYVYCAKYPYVYGTSHWYFDVWGQT 112

RESULT 11
US-09-136-389-126
Sequence 126, Application US/09136389
Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studulka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360

FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-126

Query Match 77.1%; Score 507.5; DB 3; Length 118;
Best Local Similarity 77.8%; Pred. No. 2.1e-44;
Matches 91; Conservative 12; Mismatches 9; Indels 5; Gaps 1;
QY 1 EVOLVSGGGLVOPGSLRLSCAASGYDFTHYGMNVVROAPGKLEWVGINTYGEPT 60
DB 1 EIQLVSGGGLVPGGSVRLSCAASGYFTTNGMNVVROAPGKLEWVGINTHTEPT 60
QY 61 AADFKRFTFSLDTSKSTAYLQNSLRADTAAYVYCAKYPYVYGTSHWYFDVWGQT 117
DB 61 ADFKRFRTFSLDTSKSTAYLQNSLRADTAAYVYCAKYPYVYGTSHWYFDVWGQT 112

RESULT 12
US-09-610-838-126
Sequence 126, Application US/09610838
Patent No. 6376217
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studulka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-610-838-126

Query Match 77.1%; Score 507.5; DB 3; Length 118;
Best Local Similarity 77.8%; Pred. No. 2,1e-44;
Matches 91; Conservative 12; Mismatches 9; Indels 5; Gaps 1;
QY 1 EVLVESGGGLVPGGSLRLSCAASGYDFTHYGMMWRQAPGKLEWGMINTYTGERTY 60
DB 1 EIQLVGGGGLVPRGGSVRISCAASGYTFYNYGMMWRQAPGKLEWGMINTYTGERTY 60
QY 61 AADFKRFTSLDPSKSTAYLQWNSLRAPDAVYCAKPYPGYGTSHVYFPMGCGT 117
DB 61 ADFKGRFTSLDPSKSTAYLQWNSLRAPDAVYCAKPYPGYGTSHVYFPMGCGT 112

RESULT 13
US-09-711-485-126
Sequence 126, Application US/09711485
Patent No. 6649742
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-711-485-126

Query Match 77.1%; Score 507.5; DB 4; Length 118;
Best Local Similarity 77.8%; Pred. No. 2,1e-44;
Matches 91; Conservative 12; Mismatches 9; Indels 5; Gaps 1;
QY 1 EVLVESGGGLVPGGSLRLSCAASGYDFTHYGMMWRQAPGKLEWGMINTYTGERTY 60
DB 1 EIQLVGGGGLVPRGGSVRISCAASGYTFYNYGMMWRQAPGKLEWGMINTYTGERTY 60
QY 61 AADFKRFTSLDPSKSTAYLQWNSLRAPDAVYCAKPYPGYGTSHVYFPMGCGT 117
DB 61 ADFKGRFTSLDPSKSTAYLQWNSLRAPDAVYCAKPYPGYGTSHVYFPMGCGT 112

RESULT 14
US-08-488-113B-147
Sequence 147, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995

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OM protein - protein search, using sw model

Run on: March 14, 2005, 20:22:02 ; Search time 43.9912 Seconds
(without alignments)
884.760 Million cell updates/sec

Title: US-09-723-752b-116

Perfect score: 658
Sequence: 1 EVOLVESGGGLVQPGCSURL.....YPIYYGTSHWYDVGQGLT 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	658	100.0	118	9	US-09-056-160B-118
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4	658	100.0	118	14	US-10-234-671-116
5	658	100.0	123	13	US-10-153-159-3
6	658	100.0	123	13	US-10-153-176-3
7	658	100.0	123	15	US-10-443-134A-3
8	658	100.0	123	16	US-10-723-434-56
9	658	100.0	224	16	US-10-379-392-136
10	658	100.0	224	16	US-10-379-392-138
11	658	100.0	224	16	US-10-379-392-140
12	658	100.0	476	14	US-10-020-786-11
13	658	100.0	476	17	US-10-697-995-9

14	654	99.4	117	16	US-10-379-392-58
15	653	99.2	224	16	US-10-379-392-148
16	650	98.8	117	16	US-10-379-392-122
17	649	98.6	118	9	US-09-056-160B-112
18	649	98.6	118	14	US-10-234-671-110
19	649	98.6	118	15	US-10-624-153-97
20	648	98.5	224	16	US-10-379-392-156
21	645	98.0	117	16	US-10-379-392-124
22	645	98.0	231	15	US-10-364-953-5
23	644	97.9	123	16	US-10-723-434-103
24	641	97.4	117	16	US-10-379-392-130
25	640	97.3	118	9	US-09-056-160B-114
26	640	97.3	118	14	US-10-234-671-112
27	640	97.3	231	15	US-10-364-953-5
28	638	97.0	123	15	US-10-443-134A-128
29	638	97.0	123	16	US-10-723-434-105
30	635	96.5	118	9	US-09-056-160B-108
31	635	96.5	118	14	US-10-234-671-7
32	635	96.5	118	14	US-10-234-671-106
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34	635	96.5	123	9	US-09-056-160B-7
35	635	96.5	123	13	US-10-153-159-1
36	635	96.5	123	13	US-10-153-159-14
37	635	96.5	123	14	US-10-153-176-1
38	635	96.5	123	14	US-10-153-176-14
39	635	96.5	123	15	US-10-443-134A-1
40	635	96.5	123	15	US-10-443-134A-14
41	635	96.5	123	16	US-10-723-434-55
42	635	96.5	123	17	US-10-877-532-8
43	635	96.5	231	15	US-10-364-953-2
44	633	96.2	123	15	US-10-443-134A-126
45	633	96.2	123	16	US-10-723-434-104

ALIGNMENTS

Sequence 58, App1
Sequence 148, App
Sequence 122, App
Sequence 112, App
Sequence 110, App
Sequence 97, App1
Sequence 156, App
Sequence 124, App
Sequence 9, App1
Sequence 103, App
Sequence 130, App
Sequence 114, App
Sequence 112, App
Sequence 5, App1
Sequence 128, App
Sequence 105, App
Sequence 108, App
Sequence 107, App1
Sequence 7, App1
Sequence 106, App
Sequence 96, App1
Sequence 7, App1
Sequence 14, App1
Sequence 14, App1
Sequence 14, App1
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Sequence 14, App1
Sequence 55, App1
Sequence 8, App1
Sequence 126, App
Sequence 104, App

RESULT 1
US-09-056-160B-116
Sequence 116, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Beca, Manuel
APPLICANT: Welle, Manuel
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haack, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-1608-116

Query Match 100.0%; Score 658; DB 9; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.3e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYPFTHYGMMWVROAPGKLEWVGINTYTGSEPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYPFTHYGMMWVROAPGKLEWVGINTYTGSEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYYYGTSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYYYGTSHWYFDVWGQGL 118

RESULT 2

US-09-056-1608-118
Sequence 118, Application US/090561608
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056.1608
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054.856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.
REGISTRATION NUMBER: 28.616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-1608-118

Query Match 100.0%; Score 658; DB 9; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.3e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYPFTHYGMMWVROAPGKLEWVGINTYTGSEPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYPFTHYGMMWVROAPGKLEWVGINTYTGSEPT 60

DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYPFTHYGMMWVROAPGKLEWVGINTYTGSEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYYYGTSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYYYGTSHWYFDVWGQGL 118

RESULT 3

US-10-234-671-114
Sequence 114, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234.671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-Apr-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-Apr-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44.637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-234-671-114

Query Match 100.0%; Score 658; DB 14; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.3e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYPFTHYGMMWVROAPGKLEWVGINTYTGSEPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYPFTHYGMMWVROAPGKLEWVGINTYTGSEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYYYGTSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYYYGTSHWYFDVWGQGL 118

RESULT 4

US-10-234-671-116
Sequence 116, Application US/10234671

Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-234-671-116
Query Match 100.0%; Score 658; DB 14; Length 118;
Best Local Similarity 100.0%; Pred. No. 2,3e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKGLEWVGWINTYTGSEPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKGLEWVGWINTYTGSEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYYYGTSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYYYGTSHWYFDVWGQGL 118
RESULT 5
US-10-153-159-3
Sequence 3, Application US/10153159
Publication No. US20020177170A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
Hsieh, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Caili
TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIB
FILE REFERENCE: 26050-704
CURRENT APPLICATION NUMBER: US/10/153,159

CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of matured anti-VEGF antibody
US-10-153-176-3
Query Match 100.0%; Score 658; DB 13; Length 123;
Best Local Similarity 100.0%; Pred. No. 2,4e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKGLEWVGWINTYTGSEPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKGLEWVGWINTYTGSEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYYYGTSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYYYGTSHWYFDVWGQGL 118
RESULT 6
US-10-153-176-3
Sequence 3, Application US/10153176
Publication No. US20030022240A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
Hsieh, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Caili
APPLICANT: Cao, Yicheng
APPLICANT: Liu, Shengjiang
APPLICANT: Liu, Shengjiang
TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
FILE REFERENCE: 26050-701
CURRENT APPLICATION NUMBER: US/10/153,176
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of matured anti-VEGF antibody
US-10-153-176-3
Query Match 100.0%; Score 658; DB 14; Length 123;
Best Local Similarity 100.0%; Pred. No. 2,4e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKGLEWVGWINTYTGSEPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKGLEWVGWINTYTGSEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYYYGTSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYYYGTSHWYFDVWGQGL 118
RESULT 7
US-10-443-134A-3

Sequence 3, Application US/10443134A
Publication No. US20040010376A1
GENERAL INFORMATION:
APPLICANT: Luo, Peizhi
APPLICANT: Hejeh, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Caoli
APPLICANT: Cao, Yicheng
APPLICANT: Liu, Shengjiang
TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
FILE REFERENCE: 26050-709
CURRENT APPLICATION NUMBER: US/10/443,134A
CURRENT FILING DATE: 2003-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 10/153,176
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/153,159
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of matured anti-VEGF antibody
US-10-443-134A-3

Query Match 100.0%; Score 658; DB 15; Length 123;
Best Local Similarity 100.0%; Pred. No. 2,4e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGGSRLRLSCAASGYDFTHYGMWVROAPGKLEWGMINTYTGSEPT 60
DB 1 EVOLVESGGGLVOPGGSRLRLSCAASGYDFTHYGMWVROAPGKLEWGMINTYTGSEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKYPYYGTSWYFDWVGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKYPYYGTSWYFDWVGQGL 118

RESULT 8
US-10-723-434-56
Sequence 56, Application US/10723434
Publication No. US20040133357A1
GENERAL INFORMATION:
APPLICANT: Zhong, Pingyu
APPLICANT: Luo, Peizhi
APPLICANT: Wang, Kevin C.
APPLICANT: Hejeh, Mark
APPLICANT: Li, Yan
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
FILE REFERENCE: 26050-709,501
CURRENT APPLICATION NUMBER: US/10/723,434
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 10/153,176
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/443,134
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn version 3.1
SEQ ID NO 56
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: VH
US-10-723-434-56

Query Match 100.0%; Score 658; DB 16; Length 123;
Best Local Similarity 100.0%; Pred. No. 2,4e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGGSRLRLSCAASGYDFTHYGMWVROAPGKLEWGMINTYTGSEPT 60
DB 1 EVOLVESGGGLVOPGGSRLRLSCAASGYDFTHYGMWVROAPGKLEWGMINTYTGSEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKYPYYGTSWYFDWVGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKYPYYGTSWYFDWVGQGL 118

RESULT 9

US-10-379-392-136
Sequence 136, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:

APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahlvatt, Basell I.

TITLE OF INVENTION: ANTIBODY OPTIMIZATION

FILE REFERENCE: A-71386-3 463077-236

CURRENT APPLICATION NUMBER: US/10/379,392

CURRENT FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/360,843

PRIOR FILING DATE: 2002-03-01

PRIOR APPLICATION NUMBER: US 60/384,197

PRIOR FILING DATE: 2002-05-29

NUMBER OF SEQ ID NOS: 184

SOFTWARE: PatentIn version 3.2

SEQ ID NO 136

LENGTH: 224

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Humanized

US-10-379-392-136

Query Match 100.0%; Score 658; DB 16; Length 224;
Best Local Similarity 100.0%; Pred. No. 4,1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGGSRLRLSCAASGYDFTHYGMWVROAPGKLEWGMINTYTGSEPT 60
DB 1 EVOLVESGGGLVOPGGSRLRLSCAASGYDFTHYGMWVROAPGKLEWGMINTYTGSEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKYPYYGTSWYFDWVGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKYPYYGTSWYFDWVGQGL 118

RESULT 10
US-10-379-392-138
Sequence 138, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahlvatt, Basell I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29

NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 138
LENGTH: 224
TYPE: PRT
ORGANISM: Artificial sequence
FEATURES:
OTHER INFORMATION: Synthetic
US-10-379-392-138

Query Match 100.0%; Score 658; DB 16; Length 224;
Best Local Similarity 100.0%; Pred. No. 4,1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGGSRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTYTGEPY 60
DB 1 EVOLVESGGGLVOPGGSRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTYTGEPY 60
DB 61 AADFKRRFTSLDTSKSTAYLQNMNSLRABDTAVVYCAKPYPGTSHWYFDVMGGTL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNMNSLRABDTAVVYCAKPYPGTSHWYFDVMGGTL 118

RESULT 11

US-10-379-392-140
Sequence 140, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjardais, John Rudolf
APPLICANT: Marshall, Shannon Alida
APPLICANT: Dahljat, Basel I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 140
LENGTH: 224
TYPE: PRT
ORGANISM: Artificial sequence
FEATURES:
OTHER INFORMATION: Synthetic
NAME/KEY: MISC FEATURE
LOCATION: (134)..(134)
OTHER INFORMATION: Xaa at position 134 can be Leu or Met
FEATURES:
NAME/KEY: MISC FEATURE
LOCATION: (189)..(189)
OTHER INFORMATION: Xaa at position 189 can be Val, Met, Ala or Ser
FEATURES:
NAME/KEY: MISC FEATURE
LOCATION: (191)..(191)
OTHER INFORMATION: Xaa at position 191 can be Val, Met or Ile
US-10-379-392-140

Query Match 100.0%; Score 658; DB 16; Length 224;
Best Local Similarity 100.0%; Pred. No. 4,1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGGSRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTYTGEPY 60
DB 1 EVOLVESGGGLVOPGGSRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTYTGEPY 60
QY 61 AADFKRRFTSLDTSKSTAYLQNMNSLRABDTAVVYCAKPYPGTSHWYFDVMGGTL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNMNSLRABDTAVVYCAKPYPGTSHWYFDVMGGTL 118

RESULT 12
US-10-020-786-11
Sequence 11, Application US/10020786
Publication No. US20030073164A1
GENERAL INFORMATION:
APPLICANT: Simmons, Laura C.
APPLICANT: Klimowski, Laura
APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
FILE REFERENCE: PI793R1
CURRENT APPLICATION NUMBER: US/10/020,786
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/256,164
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 11
LENGTH: 476
TYPE: PRT
ORGANISM: Artificial sequence
FEATURES:
OTHER INFORMATION: anti-VEGF heavy chain
US-10-020-786-11

RESULT 13

US-10-697-995-9
Sequence 9, Application US/10697995
Publication No. US20050048572A1
GENERAL INFORMATION:
APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION
FILE REFERENCE: 11669.195USU1
CURRENT FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: US 60/422,952
PRIOR FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 9
LENGTH: 476
TYPE: PRT
ORGANISM: Artificial sequence
FEATURES:
OTHER INFORMATION: anti-VEGF heavy chain
US-10-697-995-9

QY 1 EVOLVESGGGLVOPGGSRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTYTGEPY 60
DB 24 EVOLVESGGGLVOPGGSRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTYTGEPY 83
QY 61 AADFKRRFTSLDTSKSTAYLQNMNSLRABDTAVVYCAKPYPGTSHWYFDVMGGTL 118
DB 84 AADFKRRFTSLDTSKSTAYLQNMNSLRABDTAVVYCAKPYPGTSHWYFDVMGGTL 141

Query Match 100.0%; Score 658; DB 17; Length 476;
Best Local Similarity 100.0%; Pred. No. 8e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGGSRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTYTGEPY 60
DB 24 EVOLVESGGGLVOPGGSRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTYTGEPY 83
QY 61 AADFKRRFTSLDTSKSTAYLQNMNSLRABDTAVVYCAKPYPGTSHWYFDVMGGTL 118
DB 84 AADFKRRFTSLDTSKSTAYLQNMNSLRABDTAVVYCAKPYPGTSHWYFDVMGGTL 141

```
RESULT 14
US-10-379-392-58
; Sequence 58, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Bessli I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US/10/379,392
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Humanized
US-10-379-392-58
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Query Match          99.4%; Score 654; DB 16; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.8e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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OY      1  EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMMWRQAPGKGLBHWGMINITYGEPTY 60
Db      1  EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMMWRQAPGKGLBHWGMINITYGEPTY 60
OY      61 AADFKRRFTSLDTSKSTAYLQWNSLRADPTAVYYCAKPYYYGTSHWYFDVWGQGT 117
Db      61 AADFKRRFTSLDTSKSTAYLQWNSLRADPTAVYYCAKPYYYGTSHWYFDVWGQGT 117
```

```
RESULT 15
US-10-379-392-148
; Sequence 148, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Bessli I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US/10/379,392
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 148
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (5)..(5)
; OTHER INFORMATION: Xaa at position 5 can be Val or Arg
; NAME/KEY: MISC FEATURE
; LOCATION: (132)..(132)
```

```
; OTHER INFORMATION: Xaa at position 132 can be Phe or Arg
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (180)..(180)
; OTHER INFORMATION: Xaa at position 180 can be Leu, Asp, Glu, Asn, Gln, or Arg
US-10-379-392-148
```

```
Query Match          99.2%; Score 653; DB 16; Length 224;
Best Local Similarity 99.2%; Pred. No. 1.1e-46;
Matches 117; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1  EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMMWRQAPGKGLBHWGMINITYGEPTY 60
Db      1  EVQLVESGGGLVQPGGSLRLSCAASGYDFTHYGMMWRQAPGKGLBHWGMINITYGEPTY 60
OY      61 AADFKRRFTSLDTSKSTAYLQWNSLRADPTAVYYCAKPYYYGTSHWYFDVWGQGT 118
Db      61 AADFKRRFTSLDTSKSTAYLQWNSLRADPTAVYYCAKPYYYGTSHWYFDVWGQGT 118
```

```
Search completed: March 14, 2005, 20:42:13
Job time : 44.9912 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: March 14, 2005, 20:39:29 ; Search time 17.8553 Seconds
(without alignments)
635,867 Million cell updates/sec

Title: US-09-723-752b-116

Perfect score: 658
Sequence: 1 EVQLVESGGGLVQPGGSLRL...YPPYGTSHMYPDWGQGTLL 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	427	64.9	138 2 S31666	Ig heavy chain V r
2	426	64.7	123 2 S31114	Ig heavy chain - h
3	426	64.7	131 2 S26792	Ig heavy chain V r
4	424	64.4	119 2 S31107	Ig heavy chain - h
5	418.5	63.6	120 2 B42848	Ig heavy chain V r
6	418.5	63.6	128 2 S48797	Ig heavy chain V r
7	418.5	63.6	146 4 S33905	Ig heavy chain pre
8	418	63.5	125 2 S30531	Ig heavy chain V r
9	416	63.2	123 2 S26794	Ig heavy chain V r
10	416	63.2	142 2 S19245	Ig heavy chain pre
11	415	63.1	127 2 S38489	Ig heavy chain - h
12	415	63.1	140 2 S31686	Ig heavy chain V r
13	414	62.9	140 2 S31686	Ig heavy chain V r
14	413.5	62.8	140 2 S70442	Ig heavy chain pre
15	412	62.6	119 2 A53285	Ig heavy chain V a
16	411.5	62.5	115 2 S19668	Ig heavy chain V r
17	411	62.5	121 2 S19666	Ig heavy chain V r
18	411	62.5	121 2 S31104	Ig heavy chain (su
19	411	62.5	160 2 S05271	Ig heavy chain pre
20	410.5	62.4	147 2 S37780	Ig variable region
21	409.5	62.2	119 2 S37453	Ig mu chain - huma
22	409	62.2	119 2 S31108	Ig heavy chain - h
23	408	62.0	119 2 D36005	Ig heavy chain V r
24	408	62.0	121 2 S56673	Ig heavy chain - h
25	407.5	61.9	114 2 D32667	Ig heavy chain V r
26	407	61.9	135 2 S31598	Ig heavy chain V r
27	407	61.9	143 2 S23624	Ig heavy chain V r
28	406.5	61.8	114 2 C32967	Ig heavy chain V r
29	406.5	61.8	124 2 S20782	Ig heavy chain V r

30	406	61.7	132 2 S31603	Ig heavy chain V r
31	405	61.6	120 1 M3HUBW	Ig heavy chain V-1
32	405	61.6	121 2 S31113	Ig heavy chain - h
33	402.5	61.2	120 2 S48798	Ig heavy chain V r
34	402	61.1	119 2 C36005	Ig heavy chain V r
35	401.5	61.0	124 1 AWM551	Ig heavy chain V r
36	401.5	61.0	128 1 S26786	Ig heavy chain V r
37	401.5	61.0	141 2 S31669	Ig heavy chain V r
38	401	60.9	117 2 S31109	Ig heavy chain - h
39	401	60.9	117 2 S36259	Ig heavy chain VH1
40	400	60.8	123 1 AVMST5	Ig heavy chain V r
41	399.5	60.7	120 2 S25789	Ig heavy chain V r
42	399.5	60.7	122 2 S31117	Ig heavy chain - h
43	399	60.6	117 2 S32190	Ig heavy chain V r
44	399	60.6	123 2 PL0017	Ig heavy chain V-D
45	399	60.6	136 2 S35759	BHD9D10 protein -

ALIGNMENTS

RESULT 1

S31666 Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence _revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31666

R/Submitter: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31666

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-118 <CUI>

A/Cross-references: EMBL:214202; NID:g30963; PIDN:CAA78571.1; PID:g30964

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heterodimer; immunoglobulin

F/34-117/Domain: immunoglobulin homology <IMM>

Query Match Score 427; DB 2; Length 138;

Best Local Similarity 70.3%; Pred. No. 1.3e-32;

Matches 83; Conservative 9; Mismatches 22; Indels 4; Gaps 1;

Qy	1	EVQLVESGGGLVQPGGSLRLSCAASGYPFTHYGMNWQAQPGKLEWVGWINTYGEPTY 60
Db	20	EVQLVESGGGLVQPGGSLRLSCAASGYPFTSYAMSVNRQAPGKLEWVSAISGSGSTYY 79
Qy	61	AADFKRFTFSLDTSKSTAYLQNSLRADTAVYTCAKTPYYGTSHTYFDWGQGTLL 118
Db	80	ADVSKRFTISRDNKNTLYLQNSLRADTAVYCAK----ARTGYWFDLWGRGRTL 133

RESULT 2

S31114 Ig heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence _revision 26-May-1995 #text_change 17-Mar-1999

C/Accession: S31114

R/Submitter: F.M.; Timmer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar

Bur. J. Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple

A/Reference number: S31104; M01D:92111633; PMID:1730252

A/Accession: S31114

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-123 <PDA>

A/Cross-references: EMBL:X62963

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heterodimer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Best Local Similarity 69.1%; Pred. No. 7, 6e-32;
Matches 85; Conservative 10; Mismatches 21; Indels 7; Gaps 3

Qy	1	EVQLVESGGGLVPGQSLRLISCAASGYDFTTHGMMVRRQAPKGLIEWMTINTYGETTY	60
Db	1	QVQLVESGGGVVQPGHSLRLISCAASGFTSSVGMHVRQAPEKGLIEWAVI-WTIDGSKNY	59
Qy	61	AAR-FKRRFTFLDSKSTAYLQMSNLRAEDPAVYVCAKPYRYGTSIMYF-----DYWG	114
Db	60	YADSVKGRFTISDNKSNTLLYLOMSNLRAEDPAVYICANDNTYYISDSGLIYYIGDMWG	119
Qy	115	QGT	117
Db	120	QGT	122

```

RESULT 7
S33905
IG heavy chain precursor V region - synthetic
C/Species: synthetic
C/Date: 13-Jan-1995 #sequence_revision 30-Apr-1998 #text_change 20-Oct-2000
C/Accession: S33905
R/Lin, A.Y.; Robinson, R.R.; Hellstroem, K.E.; Murray Jr., E.D.; Chang, C.P.; Hellstroem
Proc. Natl. Acad. Sci. U.S.A. 84, 3439-3443, 1987
A/Title: Chimeric mouse-human IgG1 antibody that can mediate lysis of cancer cells.
A/Reference number: S33905; MUID:87204152; PMID:3106970
A/Accession: S33905
A/Molecule type: mRNA
A/Residues: 1-146 <Lit>
A/Cross-references: EMBL:M16072; NID:g195270; PIN:AAA8229.1; PID:g195271

```

```

Qy      63.6%; Score 418.5; DB 4; Length 146;
Best Local Similarity 64.1%; Pred. No. 8.7e-32;
Matches 75; Conservative 20; Mismatches 19; Indels 3; Gaps 2.

Qy      1  EVQLVESGGGLVPGGSLRLSCAASGYDFTHTGNNMVAQAPKGLEMTVGTINTYGPETY 60
        :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      20  QIQLVSGSPELKKRGETIVKISCKKSGYFTFTIGNMMVKQAPKGLKMMGMINTYIGPTY 79
        :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy      61  AAEKKRRFTSLDTSKSTAYLQNMNLSRAEDTAVVYCAKPYPYGSHMYFDVWGCGT 117
        :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      80  ADDPKGFAFSLERISATYAIQINLKKEDNATYICAFPS--YGNRS-YSDIWGCGT 133
        :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

```

RESULT 8
S30531
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S30531
R/Mariette, X.
submitted to the EMBL Data Library, October 1992
A/Reference number: S30520
A/Accession: S30531
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-125 <MAR>
A/Cross-references: UNIPROT:Q9UL91; EMBL:Z18317
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
I:15-98/Domain: immunoglobulin homology <IIMV>

```

	Query Match	Similarity	63.5%	Score 418	DB 2	Length 125
	Best Local	86.7%	Pred. No. 8,2e-32			
	Matches	80	Conservative	14	Mismatches	24
					Indels	2
					Gaps	1
Qy	1	EVOLVEGGGIVVPGSGSLRLCSAAGYDDTHYKGMNMPRA	PKKGLKEMVCMITTYGCEPY	60		
Db	1	EVOLVESGGGLVPGSGSLRLCSAAGFTFSISMMNKPRAFGKLE	MSITLISSSSSTIRY	60		
Qy	61	AADFGRRTFLSDTSKSTAYLQMSLRADETAVYVCAYKPY	YGTSHW--YFDVMGQGL	118		
Db	61	ADVSVGRRTISDNNKNSLYLQMSLRADETAVYVCARRNVD	SGSYSHYDYGQGL	120		

```

RESULT 9
S26794
IG heavy chain V region - human
C.Species: Homo sapiens (man)
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
R.Accession: S26794
R.Motzart, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A.Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fa
A.Reference number: S26786; MUID:9211632; PMID:1730251
A.Accession: S26794
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-123 <MOB>
A.Cross-references: EMBL:X61011
C.Superfamily: Immunoglobulin V region; immunoglobulin homology
C.Keywords: heterodictamer; immunoglobulin
F.15-98/Domain: immunoglobulin homology <IM>

```

Query Match	63.2%;	Score 416;	DB 2;	Length 123;
Best Local Similarity	67.5%;	Pred. No. 1, 28-31;		
Matches	79;	Conservative 13;	Mismatches 25;	Indels 0; Gaps 0;

CY	1	EVOLVESGGGIVPGGSLRLTSCAAGYDVFPHYGNWNRQAPGKLELVGMINTGTGERTY	60
DB	1	EVOLVESGGGIVPGGSLRLTSCAAGSTFSSISNNWRQAPGKLELVSYISSSSRITTY	60
		
CY	61	AADFKRPTSLDTSKSTAYLQNNLSFAEDTAYTTCAKTPTTYTGTSMTVPDVMGGT	117
DB	61	ADVKGFTLSRDAAKSLYLQNNLSLDEDTAYTTCARSLKYDENYGGMDVWGCGT	117
		

```

RESULT 10
S19245
Ig heavy chain precursor V region (10P1) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C/Accession: S19245
R/Riktkham, F.M.; Mortari, F.; Newton, J.A.; Schroeder, H.W.
E/BO V. 11, 603-609, 1992
A/Title: Immunoglobulin V (H) clan and family identity predicts variable domain structure
A/Reference number: S19245; MUID:92164649; PMID:1537339
A/Accession: S19245
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-142 <KIR>
A/Cross-references: EMBL:X59906; NID:g37791; PIDD:CAA42547.1; PID:g37792
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; Immunoglobulin
C/Key117/Domain: Immunoglobulin homology <IMV>

```

Query Match 63.2%; Score 416; DB 2; Length 142;
Best Local Similarity 66.1%; Pred. No. 1.4e-31;
Matches 78; Conservative 14; Mismatches 26; Indels 0; Gaps 0;

Cy 1 EVOLVESGGGLVPGGSLRLVLSCAASGYDPLFHIGNMVRQAPGKGLFENVGINTYTGRTY 60
Db 20 QVQLVQASAEELKRGASVYSCRASGTFITFSYAMNWRQAPGQLEHMGKINTITGNTPTF 79
61 AADFKRRFTSLDTSKSTAYLQNNSLPAEDTAVYYCAKPPYYGTSTHMYEDVWGQGL 118
Cy 80 AAGGTGFVSLDTSVSTAYLQISSLAEDTAVYYCARATLMMTAVATHPEFWQGL 137
Db

```

RESULT 11
S38489
IG heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #ext_change 23-Jul-1999
C:Accession: S38489
C:Markers: J.D.: Ouweland, W.H.: Bye, J.M.: Finnern, R.: Gorlick, B.D.: Voak, D.: Thorpe,

```


Best Local Similarity 64.4%; Pred. No. 2.8e-31;
Matches 76; Conservative 16; Mismatches 20; Indels 6; Gaps 2;

```
QY      1 EVQLVESGGGLVQPGGSLRLSCAASGYPFTHYGMNWVRQAPGKGLEWVGMINTYTGEPY 60
      ::|||::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 QIQLVQSGPELKKPGETVKISKASGYFTYNGMMWVKQAPGKGLEWMDWINTYTGEPY 60
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY      61 AADFKRRFTPELDTSKSTAYLQMNLSRAEDTAVYYCAKYPYYGTSHWY-PDWWGGGT 117
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 AADFKRRFAPFSLTSASTAYLQINDLKNEDTATYFCAR-----GNRVYVYAMDYWGQGT 113
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
```

Search completed: March 14, 2005, 21:08:52
Job time : 17.8553 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2005, 20:32:33 / Search time 82.807 Seconds

(without alignments)
729.713 Million cell updates/sec

Title: US-09-723-752B-116

Sequence: 1 EVOLVSGGGLVQPGGSLRL.....YPPYGTSHMYFPDWGQCTL 118

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	414.5	63.0	475	2	Q6MZ06
2	414	62.9	597	2	Q96BB9
3	413.5	62.8	241	2	Q921A6
4	406.5	61.8	118	2	Q9UL91
5	405	61.6	120	1	HV3E_HUMAN
6	404.5	61.5	122	1	HV21_MOUSE
7	402.5	61.2	605	2	Q6GMT2
8	401.5	61.0	573	2	Q8WUJ8
9	400	60.8	123	1	HV18_MOUSE
10	399	60.6	113	2	Q9UL90
11	398	60.5	123	1	HV19_MOUSE
12	398	60.5	472	2	Q6N0B9
13	396.5	60.3	473	2	Q6MZV7
14	395.5	60.1	112	2	Q9HCCI
15	395.5	60.1	613	2	Q8WUK1
16	394	59.9	478	2	Q6P181
17	391	59.4	123	1	HV22_MOUSE
18	391	59.2	240	2	Q6S2C9
19	389.5	59.2	544	2	Q6RJ95
20	389	59.1	123	1	HV23_MOUSE
21	389	59.1	125	2	Q6P1D0
22	389	59.1	470	2	Q6PJA4
23	388.5	59.0	119	1	HV38_MOUSE
24	387	58.8	121	2	Q9UL71
25	386	58.7	464	2	Q6MZU6
26	384.5	58.4	122	1	HV20_MOUSE
27	384	58.4	487	2	Q80Z17
28	382	58.1	499	2	Q8NSK4
29	381	57.9	115	1	HV3D_HUMAN
30	381	57.9	123	1	HV24_MOUSE
31	379.5	57.7	119	1	HV37_MOUSE

32	379.5	57.7	147	2	Q9Y509	Q9Y509 homo sapien
33	379.5	57.7	487	2	Q6ZYX0	Q6ZYX0 homo sapien
34	378.5	57.5	493	2	Q6MZ9	Q6MZ9 homo sapien
35	378	57.4	493	2	Q6GMX2	Q6GMX2 homo sapien
36	375.5	57.1	122	1	HV3G_HUMAN	Q91768 homo sapien
37	375	57.0	123	1	HV25_MOUSE	P01794 mus musculu
38	374.5	56.9	119	1	HV40_MOUSE	P01810 mus musculu
39	374	56.8	484	2	Q99LA6	Q99LA6 mus musculu
40	374	56.8	485	2	Q6PDB8	Q6PDB8 mus musculu
41	372.5	56.6	116	2	Q683Y8	Q683Y8 mus musculu
42	372.5	56.6	118	2	Q9UL72	Q9UL72 homo sapien
43	372.5	56.6	122	2	Q9UL84	Q9UL84 homo sapien
44	372.5	56.6	136	1	HV16_MOUSE	P01783 mus musculu
45	371	56.4	470	2	Q7TWK1	Q7TWK1 mus musculu

ALIGNMENTS

RESULT 1		ALIGNMENTS	
Q6MZ06	PRELIMINARY;	PRT;	475 AA.
AC	Q6MZ06;		
DT	05-JUL-2004 (TREMblrel. 27, Created)		
DT	05-JUL-2004 (TREMblrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMblrel. 27, Last annotation update)		
DE	Hypothetical protein DKFZp686G1190.		
GN	Name=DKFZp686G1190;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX	NCBI_TaxID:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	T1SSUE=Human esophagus tumor;		
RG	The German Human cDNA Consortium;		
RA	Lauber J., Bahr A., Mewes H.W., Well B., Amid C., Osanger A., Fobo G.,		
RA	Han M., Wiemann S.,		
RL	Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BX640947; CAE45972.1; -		
DR	HSSP; P01861; IADQ.		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG_1like.		
DR	InterPro; IPR003597; IG_c1.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_v.		
DR	PIfam; PF07654; C1-set; 3.		
DR	SMART; SM00409; IG; 2.		
DR	SMART; SM00407; IGc1; 3.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 4.		
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.		
KW	Hypothetical protein.		
SQ	SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;		
Query Match			
Best Local Similarity 63.0%; Score 414.5; DB 2; Length 475;			
Matches 83; Conservative 13; Mismatches 21; Indels 5; Gaps 3;			
QY	1	EVOLVSGGGLVQPGGSLRLCAAGYDFTHYGNVWROAPGKGLVWGVNINFTGSPY	60
DB	20	EVOLVSGGGLVQPGGSLRLCAAGYDFTHYGNVWROAPGKGLVWGVNINFTGSPY	78
QY	61	AAD-FRRKFTSDTSKSTAYLQNSLRADTAIVYCAK--YPPYGTSHMYFPDWGQG	116
DB	79	YADSVKGRFTISDINTNTLYLQNSLRADTAIVYCAKADYRDYQVSPAWYFPDWGRG	138
QY	117	TL 118	
DB	139	TL 140	
RESULT 2			

```

096BB9
ID 096BB9 PRELIMINARY; PRT; 597 AA.
AC 096BB9
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marubina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fehey J., Helton E., Kesteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Krzywnicki M.I., Skalka U., Smallos D.E., Scherch A., Schin J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAH15760.1; -.
DR PIR; S05271; S05271.
DR PIR; S24260; S24260.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKOWN 3.
SQ SEQUENCE 597 AA; 65039 MW; 4FC3AD8EC263D9 CRC64;

Query Match 62.9%; Score 414; DB 2; Length 597;
Best Local Similarity 70.0%; Pred. No. 1,1e-34;
Matches 84; Conservative 5; Mismatches 29; Indels 2; Gaps 1;

QY 1 EVLVESGGGLVOPGSLRLSCAASGYDFTYHGMMWVQAQPGKLEWVGINITYTGPPT 60
DB 20 EVLVESGGGLVOPGSLRLSCAASGYDFTYHGMMWVQAQPGKLEWVGINITYTGPPT 79
QY 61 AADFKRFTSLDTSKSTAYLQMSLRADTAAYVCAKYPYVYGTSHWYF--DVGQGT 118
DB 80 AADFKRFTSLDTSKSTAYLQMSLRADTAAYVCAKYPYVYGTSHWYF--DVGQGT 139

RESULT 3
ID 0921A6 PRELIMINARY; PRT; 241 AA.
AC 0921A6
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

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DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL; U88067; AAB48044.1; -.
DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSSP; P01607; 1BWW.
DR SMART; SM00406; IGV_2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 62.8%; Score 413.5; DB 2; Length 241;
Best Local Similarity 64.1%; Pred. No. 4.7e-35;
Matches 75; Conservative 17; Mismatches 20; Indels 5; Gaps 1;

QY 1 EVLVESGGGLVOPGSLRLSCAASGYDFTYHGMMWVQAQPGKLEWVGINITYTGPPT 60
DB 1 EVLVESGGGLVOPGSLRLSCAASGYDFTYHGMMWVQAQPGKLEWVGINITYTGPPT 60
QY 61 AADFKRFTSLDTSKSTAYLQMSLRADTAAYVCAKYPYVYGTSHWYF--DVGQGT 117
DB 61 AADFKRFTSLDTSKSTAYLQMSLRADTAAYVCAKYPYVYGTSHWYF--DVGQGT 112

RESULT 4
ID 09UL91 PRELIMINARY; PRT; 118 AA.
AC 09UL91
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
RA Wu X., Liu B., Van der Werwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -.
DR PIR; PH0875; PH0875.
DR PIR; S21205; S21205.
DR PIR; S30531; S30531.
DR HSSP; P01783; 1IGC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

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Query Match	Best Local Similarity	61.8%	Score 406.5	DB 2	Length 118
Matches 80	Conservative 11	Mismatches 22	Indels 5	Gaps 1	
Qy	1 EVOLVESSGGGLVQPGSGLRISCAGSGDYFTHYGMNMQAPGKGLIEWGMINTTYGEPY	60			
Db	1 EVOLVESSGGGLVQPGSGLRISCAGSGFFSSYNNMMVQAPGKGLIEWYSISTITITYY	60			
Qy	61 AADFKRRRTFSLDTSKSTAYLYOMNSLRADDTAVYYCAKPYGYGSHYTFDWMGGTL	118			
Db	61 ADVKRGRTTIRSDNAKNSLYLQMNSLRADDTAVYYCAR----	113			
RESULT 5					
ID	HV3E_HUMAN	STANDARD	PRT	120 AA	
AC	P01766				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DE	05-JUL-2004 (Rel. 44, Last annotation update)				
DE	Ig heavy chain V-II1 region BRO.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxId=9606;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=7111674; PubMed=65324; DOI=10.1016/0019-2791(76)90271-8;				
RA	Capra J.D., Hopper J.E.;				
RT	"Comparative studies on monocytic IgM lambda and IgG kappa from an				
RT	individual patient. III. The complete amino acid sequence of the VH				
RL	region of the IgM paraprotein."				
RT	Immunochimistry 13:995-999(1976).				
CC	-1- MISCELLANEOUS: This chain was obtained from IgM isolated from the				
CC	serum of a patient with malignant lymphoma of the Waldenström				
CC	type.				
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.				
DR	PIR; A02049; M3HUBW.				
DR	HSSP; P01783; 11GC.				
DR	GO; GO:0005576; C:extracellular; NAS.				
DR	GO; GO:0003823; P:antigen binding; NAS.				
DR	GO; GO:0006955; P:immune response; NAS.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
KW	Direct protein sequencing; Immunoglobulin V region.				
FT	DOMAIN 1 111				
FT	NON TER 120 120				
SQ	SEQUENCE 120 AA; 13227 MW; D3F0428F7C2B6410 CR664;				
Query Match					
Best Local Similarity		61.6%	Score 405	DB 1	Length 120
Matches 83	Conservative 8	Mismatches 20	Indels 16	Gaps 3	
Qy	1 EVOLVESSGGGLVQPGSGLRISCAGSGDYFTHYGMNMQAPGKGLIEWGMINTTYGEPY	60			
Db	1 EVOLVESSGGGLVQPGSGLRISCAGSGFFSSYNNMMVQAPGKGLIEWYSISTITITYY	59			
Qy	61 AADFKRRRTFSLDTSKSTAYLYOMNSLRADDTAVYYCAKPY-----	111			
Db	60 ADVKRGRTTIRSDNAKNSLYLQMNSLRADDTAVYYCARSPVSLVDMGLYYTIGS-----	113			
Qy	112 VMGGGTL 118				
Db	114 VMGGGTL 120				
RESULT 6					
ID	HV21_MOUSE	STANDARD	PRT	122 AA	

AC	P01790;1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	05-JUN-2004 (Rel. 44, Last annotation update)
DE	Ig heavy chain V region M511.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE
RX	MEDLINE=81054880; PubMed=6776528;
RT	Robinson E.A., Appella E.;
RA	"Complete amino acid sequence of a mouse immunoglobulin alpha chain
RL	(MOPC 511)." ;
RU	Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980) .
CC	-I- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC	binds phosphorylcholine.
CC	-I- SIMILARITY: Contains 1 Immunoglobulin-like domain.
DR	HSSP; P01789; IMCP.
DR	InterPro; IPR007110; Ig_1like.
DR	InterPro; IPR003596; Ig_V.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SMO0406; IgV; 1.
DR	PROSITE; PSS0835; IG_LIKE; 1.
KW	Direct protein sequencing; Immunoglobulin V region.
FT	DOMAIN 1 114
FT	NON TER 122 122
SO	SEQUENCE 122 AA; 13652 MW; 9F4837731EA50207 CRC64;
Query Match	61.5%; Score 404.5; DB 1; Length 122;
Best Local Similarity	65.3%; Pred. No. 1.9e-34;
Matches	79; Conservative 13; Mismatches 20; Indels 9; Gaps 3
OY	1 EVOLVESGGGVQPGSGSLRLSCAASGVDFTHYGMNWVARQAPKGLSENV----GWINTYTG 56
DB	1 EVKLVEGGGIVQPGSGSLRLSCLATSGFTFSDFVEMWRQSPGKLEWTIAASNKANDDYT 60
OY	57 EPTYYADPKRRFTPLDTSKSTAYLQWNLSLRADTAVYYCAKPYRYYSITSHYPFWMGQ 116
DB	61 E--YSASVKGRFIVSRDPSOISLYLQNVALFAEDTAIYYCAR---YVGSSYWFDPWGAG 115
OY	117 T 117
DB	116 T 116
RESULT 7	
O6GMW2	PRELIMINARY; PRT; 606 AA.
ID	O6GMW2
AC	O6GMW2;
DT	05-JUL-2004 (TREMBLrel. 27, Created)
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT	05-JUN-2004 (TREMBLrel. 27, Last annotation update)
DE	Hypotheetical protein.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	TISSUE=Primary B-Cells;
RX	MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Straubeberg R.L., Reingold E.A., Grouse L.H., Derge J.G,
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.W., Schuler G.D.,
RA	Aleschini S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Dickchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stadleron M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein W.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loggueliano N.A., Peters G.J., Abramson R.D., Mullish S.J.,
RA	Bosak S.A., McEwan P.O., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huily S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywni M.I., Skalka U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strauberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073758; AAH73758.1; -
 DR InterPro; IPR003599; IG_1.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-sec; 4.
 DR Pfam; PF00047; IG; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG; 4.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KM Hypothetical protein.
 SQ SEQUENCE 606 AA; 66184 MW; B6B38B511464C55 CRC64;
 Query Match 61.2%; Score 402.5; DB 2; Length 606;
 Best Local Similarity 59.4%; Pred. No. 1.8e-33;
 Matches 79; Conservative 14; Mismatches 19; Indels 21; Gaps 2;
 QY 1 EVOLVESGGGLVPGGSLRLSCAASGYDFTHYGMNVRQAPGKLEWYGINITYGEPY 60
 DB 20 QVQLVESGGGLVPGGSLRLSCAASGFTSDYTHSWIRQAPGKLEWYISSSSTNY 79
 QY 61 AADFKRPFSTLSSTAYLQNMNSLRADTAAYYCAK-----PYYYG 104
 DB 80 ADSVKGFTISRDNKNSLYLQNMNSLRADTAAYYCAAGNGIAAGRVVYAAEDY 139
 QY 105 TSHWYFDWGGGT 117
 DB 140 -----MDVWGGGT 147
 RESULT 8
 ID Q8WU38 PRELIMINARY; PRT; 573 AA.
 AC Q8WU38;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strauberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073758; AAH73758.1; -
 DR InterPro; IPR003599; IG_1.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-sec; 4.
 DR Pfam; PF00047; IG; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG; 4.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KM Hypothetical protein.
 SQ SEQUENCE 606 AA; 66184 MW; B6B38B511464C55 CRC64;

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywni M.I., Skalka U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strauberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC021276; AAH21276.1; -
 DR PIR; S21205; S21205.
 DR PIR; S30532; S30532.
 DR HSSP; P18529; 118K.
 DR Pfam; PF07654; C1-sec; 2.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR SMART; SM00407; IG; 4.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KM Hypothetical protein.
 SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;
 Query Match 61.0%; Score 401.5; DB 2; Length 573;
 Best Local Similarity 65.9%; Pred. No. 2.2e-33;
 Matches 81; Conservative 9; Mismatches 22; Indels 11; Gaps 2;
 QY 1 EVOLVESGGGLVPGGSLRLSCAASGYDFTHYGMNVRQAPGKLEWYGINITYGEPY 60
 DB 20 EVQLVESGGGLVPGGSLRLSCAASGFTPDYAMHWVRQAPGKLEWVSGISWNSGIGY 79
 QY 61 AADFKRPFSTLSSTAYLQNMNSLRADTAAYYCAK-----PYYYG 114
 DB 80 ADSVKGFTISRDNKNSLYLQNMNSLRADTAAYYCAKSGSGSYIGYYG----MDVWG 134
 QY 115 QGT 117
 DB 135 QGT 137
 RESULT 9
 ID HV18 MOUSE STANDARD; PRT; 123 AA.
 AC P01787;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE (TEPC 15).
 RX MEDLINE=76222762; PubMed=819932;
 RA Rudikoff S., Potter M.;
 RT "Size differences among immunoglobulin heavy chains from
 RT phosphorylcholine-binding proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
 RN [2]
 RP SEQUENCE FROM N.A. (H107).
 RX MEDLINE=8019926; PubMed=6769593; DOI=10.1016/0092-8674(80)90089-6;
 RA Early P., Huang H., Davis M., Calame K., Hood L.;
 RT "An immunoglobulin heavy chain variable region gene is generated from
 RT three segments of DNA: VH, D and JH.";
 RL Cell 19:981-992(1980).
 RN [3]
 RP SEQUENCE (S107).

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RX MEDLINE=76110488; PubMed=813561;
RX DOI=10.1146/annurev.ge.09.120175.001513;
RX Rudnikoff S., Barstead P., Porter M., Hood L.;
RX Unpublished results, cited by:
RX Hood L., Campbell J.H., Elgin S.C.R.;
RX Annu. Rev. Genet. 9:305-353(1975).
RN [4]
RP SEQUENCE (HPCM1; HPCM2 AND HPCM3).
RX MEDLINE=81197602; PubMed=7231520;
RX Geathart P.J., Johnson N.D., Douglas R., Hood L.;
RX "IgG antibodies to phosphorylcholine exhibit more diversity than their
RX IGM counterparts.";
RX Nature 291:29-34(1981).
CC -1- MISCELLANEOUS: All those sequence appears to be identical.
CC -1- MISCELLANEOUS: These chains were isolated from myeloma and
CC -1- MISCELLANEOUS: These chains that bind phosphorylcholine.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93804; AVMST5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 114
FT NON_TER 123
SQ SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;

Query Match 60.8%; Score 400; DB 1; Length 123;
Best Local Similarity 65.3%; Pred. NO. 5.8e-34;
Matches 79; Conservative 12; Mismatches 22; Indels 8; Gaps 3;

QY 1 EVOLVSGGGLVQPGGSLRLSCAAGYDPTFGMMWVRQAPGKGLIEWV---GMINTYTG 56
DB 1 EVKLVESGGGLVQPGGSLRLSCATSGFTPSDFYMEWRQPPGKLEWIAASRNKNDYTT 60
QY 57 EPTVAADFKRRFTSLDTSKSTAYLQNMNSLRADPTAVYCAKPYRYGTSHWYFPVWGQG 116
DB 61 E--YSASYKGRFIVSRDTSQSILYQNMNLRADPTAVYCAR--DYGSBSYWFVWGAG 116
QY 117 T 117
DB 117 T 117

RESULT 10
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RX [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614914; DOI=10.1006/clin.1998.4531;
RX Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berney S.M.,
RX Young D.C.;
RX "Myosin-reactive autoantibodies in rheumatic carditis and normal
RX fetus.";
RX Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -
DR PIR; S78486; S78486.
DR HSSP; P01772; 2F84.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SMO0406; IGV; 1.

```

```

DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57EPDD19086D07F CRC64;

Query Match 60.6%; Score 399; DB 2; Length 113;
Best Local Similarity 69.7%; Pred. NO. 6.7e-34;
Matches 83; Conservative 6; Mismatches 18; Indels 12; Gaps 3;

QY 1 EVOLVSGGGLVQPGGSLRLSCAAGYDPTFGMMWVRQAPGKGLIEWVGMINTYGEPT 60
DB 1 EVOLVSGGGLVQPGGSLRLSCAAGFTFSSYGMHWVRQAPGKGLIEWAFIR-YDGSNXY 59
QY 61 AAD-FKRRFTSLDTSKSTAYLQNMNSLRADPTAVYCAKPYRYGTSHWYFPVWGQTL 118
DB 60 YADSVKGRFTISRDNSKNTLYQNMNSLRADPTAVYCAKDLNY-----WQGGTL 108

RESULT 11
HVL9 MOUSE
ID HVL9 MOUSE STANDARD; PRT; 123 AA.
AC P01788;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V region H8.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RX [1]
RX SEQUENCE.
RX Barstead P.;
RX Theis (1975), California Institute of Technology / Pasadena, U.S.A.
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds phosphorylcholine.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 114
FT NON_TER 123
SQ SEQUENCE 123 AA; 13805 MW; 9D581401912F7000 CRC64;

Query Match 60.5%; Score 398; DB 1; Length 123;
Best Local Similarity 65.3%; Pred. NO. 9.4e-34;
Matches 79; Conservative 11; Mismatches 23; Indels 8; Gaps 3;

QY 1 EVOLVSGGGLVQPGGSLRLSCAAGYDPTFGMMWVRQAPGKGLIEWV---GMINTYTG 56
DB 1 EVKLVESGGGLVQPGGSLRLSCATSGFTPSDFYMEWRQPPGKLEWIAASRNKNDYTT 60
QY 57 EPTVAADFKRRFTSLDTSKSTAYLQNMNSLRADPTAVYCAKPYRYGTSHWYFPVWGQG 116
DB 61 E--YSASYKGRFIVSRDTSQSILYQNMNLRADPTAVYCAR--DYGSBSYWFVWGAG 116
QY 117 T 117
DB 117 T 117

RESULT 12
Q6N089 PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686p15220.

```

GN Name=DKFZp686p15220;
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RG The German Human CDNA Consortium;
 RA Wambut R., Heubner D., Mewes H.W., Well B., Amid C., Oeanger A.,
 RA Podo G., Han M., Wiemann S.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BX640827; CAB45781.1; -;
 DR HSSP: P01861; IADO.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF07654; C1-set; 3.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IG; 1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS50835; IG LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
 DR Hypothetical protein.
 KM SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;
 SQ

Query Match 60.5%; Score 398; DB 2; Length 472;
 Best Local Similarity 66.4%; Pred. No. 4.1e-33;
 Matches 81; Conservative 7; Mismatches 24; Indels 10; Gaps 2;

QY 1 EVOLVESGGGLVQPGSRLSCAASGYPFTYGMNVRQAQPKGLEWGMINTYGEPT 60
 DB 20 EVOLVESGGGLVQPGSRLSCAASGFTPDYAMHVRQAQPKGLEWVGISWNGSIIAY 79
 QY 61 AADPFRFTSLDTSKSTAYLQNMNSLRADTAAYYCAKPY-----YYGTSNHYFPYWGQ 115
 DB 80 ADSVKGRTISRDNKNLSYLQNMNSLRADTAAYYCAKPYGHNHYG-----MDVWQ 134
 QY 116 GT 117
 DB 135 GT 136

RESULT 13
 QMZYV7
 ID 06MEV7; PRELIMINARY; PRT; 473 AA.
 AC 06MEV7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein DKFZp686C11235.
 GN Name=DKFZp686C11235;
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human small intestine;
 RG The German Human CDNA Consortium;
 RA Bloeker H., Boecker M., Mewes H.W., Well B., Amid C., Oeanger A.,
 RA Podo G., Han M., Wiemann S.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BX640853; CAB45920.1; -;
 DR HSSP: P01861; IADO.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF07654; C1-set; 3.

DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IG; 1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS50835; IG LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
 DR Hypothetical protein.
 KM SEQUENCE 473 AA; 52121 MW; 9476B4C0BFC447 CRC64;
 SQ

Query Match 60.3%; Score 396.5; DB 2; Length 473;
 Best Local Similarity 65.6%; Pred. No. 5.9e-33;
 Matches 80; Conservative 14; Mismatches 21; Indels 7; Gaps 4;

QY 1 EVOLVESGGGLVQPGSRLSCAASGYPFTYGMNVRQAQPKGLEWGMINTYGEPT 60
 DB 20 EVOLVESGGGLVQPGSRLSCAASGFTSFENMVRQAQPKGLEWLSYI-TRSGNTY 78
 QY 61 AADPFRFTSLDTSKSTAYLQNMNSLRADTAAYYCAKPYGYTSHY---PFWGQ 116
 DB 79 YADSLQGRFTISRDNKNLSYLQNMNSLRADTAAYYCARQNH--TSPYPSFPFYWGQ 136
 QY 117 TL 118
 DB 137 TL 138

RESULT 14
 QHCCI
 ID 09HCCI; PRELIMINARY; PRT; 112 AA.
 AC 09HCCI;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Single chain Fv (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB049915; BAB16829.1; -;
 DR HSSP: P01783; IIGC.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003596; IG_V.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 FT NON_TER 1
 FT NON_TER 112
 SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;
 SQ

Query Match 60.1%; Score 395.5; DB 2; Length 112;
 Best Local Similarity 66.1%; Pred. No. 1.5e-33;
 Matches 78; Conservative 9; Mismatches 24; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVQPGSRLSCAASGYPFTYGMNVRQAQPKGLEWGMINTYGEPT 60
 DB 1 EVOLVESGGGLVQPGSRLSCAASGFTFDDYGMNVRQAQPKGLEWVGISWNGSIIAY 60
 QY 61 AADPFRFTSLDTSKSTAYLQNMNSLRADTAAYYCAKPYGYTSHY---PFWGQ 118
 DB 61 ADSVKGRTISRDNKNLSYLQNMNSLRADTAAYYCARRY-----ALDTWGQTL 111

RESULT 15
 Q8WUK1
 ID 08WUK1; PRELIMINARY; PRT; 613 AA.
 AC 08WUK1;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE IGHM protein.
 OS Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toehiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywiński M.I., Skalske U., Smalhe U., Smalhe D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Straube R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC020240; AAH20240.1; -.
DR PIR: F36005; F36005.
DR PIR: G36005; G36005.
DR PIR: PH1642; PH1642.
DR PIR: PH1643; PH1643.
DR PIR: PH1644; PH1644.
DR PIR: PH1645; PH1645.
DR PIR: PL0098; PL0098.
DR PIR: PL0120; PL0120.
DR PIR: S15590; S15590.
DR PIR: S31116; S31116.
DR PIR: S31119; S31119.
DR PIR: S70442; S70442.
DR HSSP: P01861; IADQ.
DR Pfam: PF07654; C1-set; 4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG LIKE; 5.
DR PROSITE: PSS0290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;

```

Query Match 60.1%; Score 395.5; DB 2; Length 613;

Best Local Similarity 66.1%; Pred. No. 9.9e-33;

Matches 82; Conservative 9; Mismatches 18; Indels 15; Gaps 4;

```

QY 1 EVOLVESGGGLVOPGSGSLRLSCAASGYDFTHYGNMVRQAQPGKLEWVGWINTYTGPTY 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 20 QVOLVESGGGVVOPGSLRLSCAASGYDFTSYGNMVRQAQPGKLEWVAVI-SYDGSNKY 78
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AAD-FKRRFTFSLDTSKSTAYLQNSLRAEDTAVYCAKYPYYGTSHM-----YPDVWG 114
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 79 YADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYCAK-----DWSBGVETFDIWG 130
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 115 QGTL 118
DB :|||||:
QY 131 QGTM 134
DB :|||||:

```

Search completed: March 14, 2005, 20:49:19
Job time : 82.807 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 14, 2005, 20:39:29 ; Search time 17.8553 Seconds

(without alignment)

Title: US-09-723-752B-7

Perfect score: 655
Sequence: 1 EVQLVDSGGGLVQPGGSLRL...YFHYGSSHWYFDVWGQCTL 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	433	66.1	119	2 S31107	Ig heavy chain - h
2	432	66.0	123	2 S31114	Ig heavy chain - h
3	432	66.0	125	2 S30531	Ig heavy chain V r
4	431.5	65.9	140	2 S70442	Ig heavy chain pre
5	431	65.8	138	2 S31666	Ig heavy chain V r
6	430.5	65.7	120	2 B42848	L6 mAb heavy chain
7	430.5	65.7	146	4 S33905	Ig heavy chain pre
8	430	65.6	131	2 S26792	Ig heavy chain V r
9	428	65.3	140	2 S31588	Ig heavy chain V r
10	426	65.0	123	2 S26794	Ig heavy chain V r
11	426	65.0	127	2 S38489	Ig heavy chain - h
12	424.5	64.8	128	2 S48797	Ig heavy chain V r
13	424	64.7	119	2 A53285	Ig heavy chain V a
14	423.5	64.7	115	2 S19968	Ig heavy chain V r
15	421	64.3	121	2 S15673	Ig heavy chain - h
16	421	64.3	142	2 S31686	Ig heavy chain V r
17	420	64.1	140	2 S19245	Ig heavy chain pre
18	419	64.0	121	2 S31104	Ig heavy chain V r
19	417.5	63.7	147	2 S37780	Ig variable region
20	417	63.7	121	2 S19666	Ig heavy chain V r
21	416.5	63.6	141	2 S31669	Ig heavy chain V r
22	415.5	63.4	114	2 D32967	Ig heavy chain V r
23	415	63.4	117	2 S36259	Ig heavy chain V r
24	415	63.4	119	2 S31108	Ig heavy chain - h
25	414.5	63.3	114	2 C32967	Ig heavy chain V r
26	414.5	63.3	122	2 E36005	Ig heavy chain V r
27	414.5	63.3	124	2 S20782	Ig heavy chain V r
28	414	63.2	119	2 D36005	Ig heavy chain V r
29	414	63.2	121	2 S31113	Ig heavy chain - h

30	414	63.2	160	2 S05271	Ig heavy chain pre
31	413.5	63.1	124	1 AVM551	Ig heavy chain V r
32	413	63.1	123	1 AVM575	Ig heavy chain V r
33	413	63.1	135	2 S31598	Ig heavy chain V r
34	413	63.1	143	2 S23624	Ig heavy chain V r
35	412.5	63.0	120	2 S48798	Ig heavy chain V r
36	412	62.9	119	2 C36005	Ig heavy chain V r
37	412	62.9	123	2 P30017	Ig heavy chain V-D
38	410.5	62.7	119	2 S37453	Ig mu chain - huma
39	410	62.6	132	2 S31603	Ig heavy chain V r
40	409.5	62.5	122	2 S26789	Ig heavy chain V r
41	409.5	62.5	122	2 S31117	Ig heavy chain - h
42	408.5	62.4	114	2 S36280	Ig heavy chain V r
43	408.5	62.4	124	2 E30539	Ig heavy chain V r
44	408	62.3	117	2 S31109	Ig heavy chain - h
45	408	62.3	124	2 P31404	Ig heavy chain V r

ALIGNMENTS

```

RESULT 1
S31107
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: S31107
R/Raaphorst, F.M.; Timmer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31107
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-119 <RAA>
A/Cross-references: EMBL:X62955
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 66.1% Score 433; DB 2; Length 119;
Matches 87; Conservative 8; Mismatches 19; Indels 4; Gaps 2;

Qy 1 EVQLVDSGGGLVQPGGSLRLCAASGYPFTNYGMNVRQAPKGLEWVGWINTYGEPT 60
Db 1 EVQLVDSGGGLVQPGGSLRLCAASGYPFTNYGMNVRQAPKGLEWVGWINTYGEPT 60

Qy 61 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQCTL 118
Db 61 ADSVGRFTISRDNKNTLYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQCTL 114

RESULT 2
S31114
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: S31114
R/Raaphorst, F.M.; Timmer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31114
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-123 <RAA>
A/Cross-references: EMBL:X62963
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

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A:Accession: S31588
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <CUI>
C:Cross-references: EMBL:Z14200; NID:930957; PIDN:CAA78569.1; PID:930958
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      65.3%; Score 428; DB 2; Length 140;
Best Local Similarity 72.9%; Pred. No. 6,1e-32;
Matches 86; Conservative 9; Mismatches 21; Indels 2; Gaps 2;

Oy      1 EVQLVESGGGVLPQGGSLRLISCAASGYTFNMGWNRQAPGKGLGVWGINTYTGPEPT 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|:|
Db      20 EVQLVESGGGVLPQGGSLRLISCAASGYTFSSYASWNRQAPGKGLGVWYSAISGSGSTYY 79
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|:|

Oy      61 AADPKRFFSLDPSKSTAYLQWNSLRADDTAVYYCAKPHYGGSSHWYPDVWGQGT 118
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|:|
Db      80 ADSVKGRFTISRDSKSTLYLQWNSLRADDTAVYYCAK-DHDY-SNVIYFDYWGQGT 135
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|:|

RESULT 10
S26794
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C:Accession: S26794
R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam
A:Reference number: S26786; MUID:92111632; PMID:11730251
A:Accession: S26794
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-123 <MOR>
C:Cross-references: EMBL:X61011
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      65.0%; Score 426; DB 2; Length 123;
Best Local Similarity 68.4%; Pred. NO. 8.2e-32;
Matches 80; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

Oy      1 EVQLVESGGGVLPQGGSLRLISCAASGYTFNMGWNRQAPGKGLGVWGINTYTGPEPT 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|:|
Db      1 EVQLVESGGGVLPQGGSLRLISCAASGYTFSSYASWNRQAPGKGLGVWYSAISGSGSTYY 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|:|

Oy      61 AADPKRFFSLDPSKSTAYLQWNSLRADDTAVYYCAKPHYGGSSHWYPDVWGQGT 117
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|:|
Db      61 ADSVKGRFTISRDAKSKSYLQWNSLRADDTAVYYCAKSIKYDYENYYGMDVWGQGT 117
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|:|

RESULT 11
S38489
Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38489
R:Marko, J.D.; Ouehand, W.H.; Bye, J.M.; Finnen, R.; Gorick, B.D.; Voak, D.; Thorpe,
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a
A:Reference number: S38488
A:Accession: S38489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <MAR>
C:Cross-references: EMBL:Z23028; NID:9414025; PIDN:CAA80563.1; PID:9414026
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

```


C:Superfamily: immunoglobulin V region; immunoglobulin homology
F,15-98/Domain: immunoglobulin homology <1M>

Query Match 64.3%; Score 421; DB 2; Length 121;
Best Local Similarity 70.3%; Pred. No. 2.3e-31;
Matches 83; Conservative 8; Mismatches 25; Indels 2; Gaps 1;

QY	1	EVOLVESGGGLVQPGGSLRLGCAAGYTFTNYGMWVROAPGKGLEWYGMINTYGEPTY	60
DB	1	EVQLVESGGGLVQPGGSLRLCTASGFTPTSGMSWROAPGKGLEWWSAISGGSTYY	60
QY	61	AADFRRFTPSLDTSKSTAYLQMSLRAEDTAVYYCAKYPHYGSSHWYFDVWGQGTL	118
DB	61	ADSVKGRFTISRDNKNTLYIQMSLRAEDTAVYYCAAPRHAGSP--YDIWGQGTL	116

Search completed: March 14, 2005, 21:08:50
Job time : 18.8553 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 14, 2005, 20:32:33 ; Search time 82.807 Seconds

(without alignments)
729.713 Million cell updates/sec

Title: US-09-723-752b-7

Perfect score: 655
Sequence: 1 EVOLVESGGGLVPGGSLRL.....YPHYGSSHWYFDVWGQCTL 118Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	425.5	65.0	475	2	Q6MZ06
2	420	64.1	597	2	Q96BB9
3	419.5	64.0	241	2	Q921A6
4	415.5	63.4	118	2	Q9UL91
5	415.5	63.4	122	1	HV21_MOUSE
6	413	63.1	123	1	HV18_MOUSE
7	410	62.6	113	2	Q9UL50
8	409	62.4	123	1	HV19_MOUSE
9	405.5	61.9	606	2	Q6GM72
10	405	61.8	120	1	HV3E_HUMAN
11	404.5	61.6	573	2	Q6MU38
12	403.5	61.6	613	2	Q6WUK1
13	402.5	61.5	473	2	Q6MZV7
14	402	61.4	123	1	HV23_MOUSE
15	401.5	61.3	112	2	Q9HCT1
16	401	61.2	123	1	HV22_MOUSE
17	401	61.2	472	2	Q6N089
18	400	61.1	240	2	Q6SZC9
19	399	60.9	470	2	Q6RJA4
20	398.5	60.8	122	1	HV20_MOUSE
21	397.5	60.7	544	2	Q6RJ55
22	397	60.6	478	2	Q6P181
23	397	60.6	487	2	Q60Z17
24	395	60.3	464	2	Q6MZU6
25	393.5	60.1	147	2	Q9Y509
26	393	60.0	121	2	Q9UL71
27	393	60.0	499	2	Q6NSK4
28	388	59.2	115	1	HV3D_HUMAN
29	388	59.2	123	1	HV24_MOUSE
30	387.5	59.2	122	1	HV3G_HUMAN
31	387.5	59.2	483	2	Q6MZX9

32	387	59.1	125	2	Q6P1L0	Q6P1L0 homo sapien
33	386	58.9	485	2	Q6PDB8	Q6PDB8 mus musculus
34	383.5	58.5	479	2	Q6MZV6	Q6MZV6 homo sapien
35	383.5	58.5	467	2	Q6ZVX0	Q6ZVX0 homo sapien
36	382	58.3	493	2	Q6GMX2	Q6GMX2 homo sapien
37	381.5	58.2	122	2	Q9UL84	Q9UL84 mus musculus
38	381	58.2	470	2	Q7TMK1	Q7TMK1 mus musculus
39	380	58.0	121	1	HV3J_HUMAN	HV3J_HUMAN homo sapien
40	379.5	57.9	119	1	HV38_MOUSE	HV38_MOUSE mus musculus
41	379	57.9	123	1	HV25_MOUSE	HV25_MOUSE mus musculus
42	378.5	57.8	118	2	Q9UL72	Q9UL72 mus sapien
43	378.5	57.8	119	1	HV37_MOUSE	HV37_MOUSE mus musculus
44	377	57.6	116	2	Q9UL53	Q9UL53 homo sapien
45	376.5	57.5	136	1	HV16_MOUSE	HV16_MOUSE mus musculus

ALIGNMENTS

RESULT 1		ALIGNMENTS	
Q6MZ06	PRELIMINARY;	PRT;	475 AA.
AC	Q6MZ06;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Hypothetical protein DKFZp686G1190.		
GN	Name=DKFZp686G1190;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Human esophagus tumor;		
RG	The German Human cDNA Consortium;		
RA	Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Oeanger A., Fobo G.,		
RA	Han M., Wiemann S.;		
RL	Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BX640947; CAE45972.1; -.		
DR	HSSP; P01861; IADQ.		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG_1like.		
DR	InterPro; IPR003597; IG_cl.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_v.		
DR	Pfam; PF07654; C1-sect; 3.		
DR	SMART; SM00409; IG; 2.		
DR	SMART; SM00407; IGcl; 3.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 4.		
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.		
KW	Hypothetical protein.		
SQ	SEQUENCE 475 AA; 52043 MW; B7EAE255A26F488E CRC64;		
Query Match			
Best Local Similarity 71.3%; Pred. No. 2.7e-36;			
Matches 87; Conservative 12; Mismatches 18; Indels 5; Gaps 4;			
QY	1	EVOLVESGGGLVPGGSLRLCAAGYFTNYGNWVROAPGKGLWVGNINTYGEPTY	60
DB	20	EVLLBSGGGLVPGGSLRLSCAAGFTFRNVMWVROAPGKGLWVGNIS-SGVNTY	78
QY	61	AAD-FKRFFSLDTSKSYVLDNMSLRADTVAYYCAK--YPHYGSS-SHWYFDVWGQ	116
DB	79	YADSVKGRFTISGDISTNLTLYQMHSIRADDTAVVYCARADYRDYQVSPAYWYFDVWG	138
QY	117	TL 118	
DB	139	TL 140	
RESULT 2			

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096BB9 ID 096BB9 PRELIMINARY; PRT; 597 AA.
AC 096BB9
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE IGM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUB=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marubina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.U., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUB=Primary B-Cells;
RA Strauberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAH15760.1; -
DR PIR; S05271; S05271.
DR PIR; S24260; S24260.
DR HSSP; P01861; IADQ.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-v.
DR Pfam; PF07654; CI-sect; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 5.
DR PROSITE; PS00290; IG-MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;

Query Match 64.1%; Score 420; DB 2; Length 597;
Best Local Similarity 70.0%; Pred. No. 1,3e-35;
Matches 84; Conservative 8; Mismatches 26; Indels 2; Gaps 1;

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DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
RX EMBL; U88067; AAB48044.1; -
DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSSP; P01607; IBMW.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 64.0%; Score 419.5; DB 2; Length 241;
Best Local Similarity 65.0%; Pred. No. 5.5e-26;
Matches 76; Conservative 18; Mismatches 18; Indels 5; Gaps 1;

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096BB9 ID 096BB9 PRELIMINARY; PRT; 597 AA.
AC 096BB9
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE IGM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUB=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marubina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.U., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUB=Primary B-Cells;
RA Strauberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAH15760.1; -
DR PIR; S05271; S05271.
DR PIR; S24260; S24260.
DR HSSP; P01861; IADQ.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-v.
DR Pfam; PF07654; CI-sect; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 5.
DR PROSITE; PS00290; IG-MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;

Query Match 64.1%; Score 420; DB 2; Length 597;
Best Local Similarity 70.0%; Pred. No. 1,3e-35;
Matches 84; Conservative 8; Mismatches 26; Indels 2; Gaps 1;

```

```

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
RX EMBL; U88067; AAB48044.1; -
DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSSP; P01607; IBMW.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 64.0%; Score 419.5; DB 2; Length 241;
Best Local Similarity 65.0%; Pred. No. 5.5e-26;
Matches 76; Conservative 18; Mismatches 18; Indels 5; Gaps 1;

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Query Match 63.4%; Score 415.5; DB 2; Length 118;
 Best Local Similarity 68.6%; Pred. No. 6.6e-36;
 Matches 81; Conservative 12; Mismatches 20; Indels 5; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGTFYFNMGMMVRAQAPGKLEWY---GWINTYTG 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGTFSSYMMWVRQAPGKLEWYSISITITTY 60
 QY 61 AADPKRRTFSLDTSKSTAYIQMNSLRADPTAVYCAKTPHYGSSHWYFDVWGQGL 118
 DB 61 ADVYKGRFTIRSDNAKNSLYIQMNSLRADPTAVYCAR-----GDSSEAFDWGQGT 113

RESULT 5

HV21_MOUSE
 ID HV21_MOUSE STANDARD; PRT; 122 AA.

AC P01790;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V region M511.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxID=10090;

RP SEQUENCE.
 RX MEDLINE=81054880; PubMed=6776528;
 RA Robinson E.A., Appelja E.;
 RT "Complete amino acid sequence of a mouse immunoglobulin alpha chain
 (MOPC 511)."
 RL Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
 CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
 CC binds phosphorylcholine.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KM Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 114
 FT NON_TER 122 122 Ig-like.
 FT SEQUENCE 122 AA; 13652 MW; 9F4837731EAS0207 CRC64;

Query Match 63.4%; Score 415.5; DB 1; Length 122;
 Best Local Similarity 66.9%; Pred. No. 6.8e-36;
 Matches 81; Conservative 13; Mismatches 18; Indels 9; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGTFYFNMGMMVRAQAPGKLEWY---GWINTYTG 56
 DB 1 EVQLVESGGGLVQPGGSLRLSCATSGTFSDPYMEWVRQPGKLEWIAASRNKANDYTT 60
 QY 57 EPTAADPKRRTFSLDTSKSTAYIQMNSLRADPTAVYCAKTPHYGSSHWYFDVWGQGL 116
 DB 61 E--YSASVKGKRFIVSRDTSQSIYLIQMNALRAEDTAIYCAR---DYGSSYWFEDVWGAG 115
 QY 117 T 117
 DB 116 T 116

RESULT 6

HV18_MOUSE
 ID HV18_MOUSE STANDARD; PRT; 123 AA.

AC P01787;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V regions TIPC 15/S107/HPCM1/HPCM2/HPCM3.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxID=10090;

RP SEQUENCE (TEPC 15).
 RX MEDLINE=76222762; PubMed=819932;
 RA Rudikoff S., Potter M.;
 RT "Size differences among immunoglobulin heavy chains from
 RT phosphorylcholine-binding proteins."
 RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
 RN [2]
 RP SEQUENCE FROM N.A. (H107).
 RX MEDLINE=80199926; PubMed=6765993; DOI=10.1016/0092-8674(80)90089-6;
 RA Early P., Huang H., Davis M., Calame K., Hood L.;
 RT "An immunoglobulin heavy chain variable region gene is generated from
 RT three segments of DNA: VH, D and JH."
 RL Cell 19:981-992(1980).
 RN [3]

RP SEQUENCE (S107).
 RX MEDLINE=76110488; PubMed=813561;
 RX DOI=10.1146/annurev.ge.09.120175.001513;
 RA Rudikoff S., Barstad P., Potter M., Hood L.;
 RL Unpublished results, cited by:
 RL Hood L., Campbell J.H., Eskin S.C.R.;
 RL Annu. Rev. Genet. 9:305-353(1975).

RP SEQUENCE (HPCM1, HPCM2 AND HPCM3).
 RX MEDLINE=81197602; PubMed=7231520;
 RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
 RT "IgG antibodies to phosphorylcholine exhibit more diversity than their
 RT IgM counterparts."
 RL Nature 291:28-34(1981).
 CC -1- MISCELLANEOUS: All those sequence appears to be identical.
 CC -1- MISCELLANEOUS: These chains were isolated from myeloma and
 CC hybridoma proteins that bind phosphorylcholine.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A93804; AVMS75.
 DR HSSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.

KM Direct protein sequencing; Hybridoma; Immunoglobulin V region.
 FT DOMAIN 1 114
 FT NON_TER 123 123 Ig-like.
 FT SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;

Query Match 63.1%; Score 413; DB 1; Length 123;
 Best Local Similarity 66.9%; Pred. No. 1.3e-35;
 Matches 81; Conservative 12; Mismatches 20; Indels 8; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGTFYFNMGMMVRAQAPGKLEWY---GWINTYTG 56
 DB 1 EVQLVESGGGLVQPGGSLRLSCATSGTFSDPYMEWVRQPGKLEWIAASRNKANDYTT 60
 QY 57 EPTAADPKRRTFSLDTSKSTAYIQMNSLRADPTAVYCAKTPHYGSSHWYFDVWGQGL 116
 DB 61 E--YSASVKGKRFIVSRDTSQSIYLIQMNALRAEDTAIYCAR---DYGSSYWFEDVWGAG 116
 QY 117 T 117
 DB 117 T 117

RESULT 7

O9U90
 ID O9U90 PRELIMINARY; PRT; 113 AA.

AC O9U90;
 DT 01-MAY-2000 (TREMURel. 13, Created)
 DT 01-MAY-2000 (TREMURel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMURel. 26, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region

DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL, AF035024; AAD56260.1; -.
 DR PIR, S78486; S78486.
 DR HSSP, P01772; 2F84.
 DR InterPro, IPR007110; IG-1like.
 DR InterPro, IPR003596; IG_v.
 DR SMART, SM00406; IGV; 1.
 DR PROSITE, PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12437 MW; ED57PDD19086D07F CRC64;

Query Match 62.6%; Score 410; DB 2; Length 113;
 Best Local Similarity 70.6%; Pred. No. 2.4e-35;
 Matches 84; Conservative 8; Mismatches 15; Indels 12; Gaps 3;

QY 1 EVLVESGGGLVQPGSLRLSCAASGTFPTNYGMNVRQAPGKGLIEWVINTYTGSEPT 60
 1 EVLVESGGGLVQPGSLRLSCAASGTFPTNYGMNVRQAPGKGLIEWVAFIR-YGSKY 59
 DB 1 EVLVESGGGLVQPGSLRLSCAASGTFPTNYGMNVRQAPGKGLIEWVAFIR-YGSKY 59
 61 AAD-FKRRTFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPHYSSHWYEDVWGQTL 118
 60 YADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYCAKADLY-----MQQGLT 108

RESULT 8
 ID HV19 MOUSE STANDARD; PRT; 123 AA.
 AC P01788;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE IG heavy chain V region H8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RA Barstead P.;
 RL Thesis (1975). California Institute of Technology / Pasadena, U.S.A.
 CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein that
 CC binds phosphorylcholine.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSSP, P01789; IMCP.
 DR InterPro, IPR007110; IG-1like.
 DR InterPro, IPR003596; IG_v.
 DR Pfam, PF00047; IG; 1.
 DR SMART, SM00406; IGV; 1.
 DR PROSITE, PS50835; IG_LIKE; 1.
 DR Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1
 FT DOMAIN 114
 FT NON_TER 123
 FT NON_TER 123
 SQ SEQUENCE 123 AA; 13805 MW; 9D581401912P7000 CRC64;

Query Match 62.4%; Score 409; DB 1; Length 123;
 Best Local Similarity 66.1%; Pred. No. 3.3e-35;
 Matches 80; Conservative 12; Mismatches 21; Indels 8; Gaps 3;
 QY 1 EVLVESGGGLVQPGSLRLSCAASGTFPTNYGMNVRQAPGKGLIEWV-----GWINTYTG 56
 1 EVLVESGGGLVQPGSLRLSCAASGTFPTNYGMNVRQAPGKGLIEWV-----GWINTYTG 56

DB 1 EVLVESGGGLVQPGSLRLSCAASGTFPTNYGMNVRQAPGKGLIEWVAFIRYDNDYTT 60
 QY 57 EPTVADPKRRTFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPHYSSHWYEDVWGQ 116
 DB 61 E-YASAVKGRFTISRDTSQSIYLQNNALRAEDTAVYCAR--DYGBSYWYEDVWGAG 116
 QY 117 T 117
 DB 117 T 117

RESULT 9
 ID Q6GMV2 PRELIMINARY; PRT; 606 AA.
 AC Q6GMV2;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Dietchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Wyere R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skelton U., Smalhe U., Smalhe D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Mair M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strauberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC073758; AAH73758.1; -.
 DR InterPro, IPR003599; IG.
 DR InterPro, IPR007110; IG-1like.
 DR InterPro, IPR003597; IG-cl.
 DR InterPro, IPR003006; IG_MHC.
 DR InterPro, IPR003596; IG_v.
 DR Pfam, PF07654; CI-sect; 4.
 DR Pfam, PF00047; IG; 4.
 DR SMART, SM00409; IG; 2.
 DR SMART, SM00407; IGV; 4.
 DR SMART, SM00406; IGV; 1.
 DR PROSITE, PS50835; IG_LIKE; 5.
 DR PROSITE, PS00290; IG_MHC; UNKNOWN_3.
 DR Hypothetical protein.
 KW Hypothetical protein.
 SQ SEQUENCE 606 AA; 66184 MW; B6B3851114E4C55 CRC64;

Query Match 61.9%; Score 405.5; DB 2; Length 606;
 Best Local Similarity 59.4%; Pred. No. 4.6e-34;
 Matches 79; Conservative 16; Mismatches 17; Indels 21; Gaps 2;
 QY 1 EVLVESGGGLVQPGSLRLSCAASGTFPTNYGMNVRQAPGKGLIEWVINTYTGSEPT 60
 1 EVLVESGGGLVQPGSLRLSCAASGTFPTNYGMNVRQAPGKGLIEWVINTYTGSEPT 60

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Db      20 QVQLVESGGGLVPGGSLRLSCAASGFTPSDYMIRCAAPKGLKLEWVSISSTSYNY 79
Qy      61 AADFKRRFTPSLDTSKSTAYLQMSLRADPTAVYCAK-----YPHYG 104
Db      80 ADSVKGRTTISRDNKNSLYLQMSLRADPTAVYCAKRGNGIAGAVRYVADYDYGG 139
Qy      105 SSHWYFDVWGCGT 117
Db      140 -----MDVWGCGT 147

RESULT 10
HV3E HUMAN STANDARD; PRT; 120 AA.
AC P01766;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region BRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=71117674; PubMed=65324; DOI=10.1016/0019-2791(76)90271-8;
RX Capra U.D., Hopper J.E.;
RT "Comparative studies on monocytic IgM lambda and IgG kappa from an
RT individual patient. III. The complete amino acid sequence of the VH
RT region of the IgM paraprotein."
RL Immunochimistry 13:995-999(1976).
CC -1- MISCELLANEOUS: This chain was obtained from IgM isolated from the
CC serum of a patient with malignant lymphoma of the Waldenstrom
CC type.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02049; M3HUBW.
DR HSBP; P01783; 118C.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 111
FT NON TER 120
SQ SEQUENCE 120 AA; 13327 MW; D3F0428F7C2B6410 CRC64;

Query Match 61.8%; Score 405; DB 1; Length 120;
Best Local Similarity 66.1%; Pred. No. 8.6e-35;
Matches 84; Conservative 7; Mismatches 20; Indels 16; Gaps 3;

Qy      1 EVOLVESGGGLVPGGSLRLSCAASGFTPSDYMIRCAAPKGLKLEWVSISSTSYNY 60
Db      1 EVOLVESGGGLVPGGSLRLSCAASGFTPSDYMIRCAAPKGLKLEWVSISSTSYNY 59
Qy      61 AADFKRRFTPSLDTSKSTAYLQMSLRADPTAVYCAK-----HYGSSHWYFD 111
Db      60 ADSVKGRTTISRDNKNSLYLQMSLRADPTAVYCAKRGNGIAGAVRYVADYDYGG 113
Qy      112 VMGQGT 118
Db      114 VMGQGT 120

RESULT 11
Q8WU38 PRELIMINARY; PRT; 573 AA.
AC Q8WU38;
DT 01-MAR-2002 (TREMBLrel. 20, Created)

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DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marzella K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Uediri T.B., Toshilyki S., Carninci P., Prange C.,
RA Baha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullishy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maiz M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL EMBL; BC021276; AAH21276.1; -
DR PIR; S21205; S21205.
DR PIR; S30532; S30532.
DR HSBP; P18529; 118K.
DR Pfam; PF07654; C1-sect; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 61.8%; Score 404.5; DB 2; Length 573;
Best Local Similarity 65.9%; Pred. No. 5.5e-34;
Matches 81; Conservative 11; Mismatches 20; Indels 11; Gaps 2;

Qy      1 EVOLVESGGGLVPGGSLRLSCAASGFTPSDYMIRCAAPKGLKLEWVSISSTSYNY 60
Db      20 EVOLVESGGGLVPGGSLRLSCAASGFTPSDYMIRCAAPKGLKLEWVSISSTSYNY 79
Qy      61 AADFKRRFTPSLDTSKSTAYLQMSLRADPTAVYCAK-----PHYGSSHWYFD 114
Db      80 ADSVKGRTTISRDNKNSLYLQMSLRADPTAVYCAKRGNGIAGAVRYVADYDYGG 134
Qy      115 QGT 117
Db      135 QGT 137

RESULT 12
Q8WU38 PRELIMINARY; PRT; 613 AA.
AC Q8WU38;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE IGHM protein.

```

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman A., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
 RA Krzywinski M.I., Skalska U., Small D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strauberg R.L.
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC020240; AAH20240.1; -
 DR PIR; F36005; F36005.
 DR PIR; G36005; G36005.
 DR PIR; PH1642; PH1642.
 DR PIR; PH1643; PH1643.
 DR PIR; PH1645; PH1645.
 DR PIR; PH1646; PH1646.
 DR PIR; PL0098; PL0098.
 DR PIR; PL0120; PL0120.
 DR PIR; S15590; S15590.
 DR PIR; S31116; S31116.
 DR PIR; S31119; S31119.
 DR PIR; S70442; S70442.
 DR HSSP; P01861; IADQ.
 DR Pfam; PF07654; Cl-sect; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;
 Query Match 61.6%; Score 403.5; DB 2; Length 613;
 Best Local Similarity 66.9%; Pred. No. 7.6e-34;
 Matches 83; Conservative 10; Mismatches 16; Indels 15; Gaps 4;
 QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYPFTNGMHWROAPGKGLIEWGINTYGEPT 60
 DB 20 QVQLVSGGTVQPSRISRSLCAAGFTFSFGKHWROAPGKGLIEWAVI-SYDGSNKY 78
 QY 61 AAD-FKRFPTSLDTSKSTAYLQNNLSLAEDTAVYCAKPHYYSRHW- -YEDVWG 114
 DB 79 YADSLQGRFTISRDNSKNTLYLQNNLSLAEDTAVYCAK- - - - -DMSGEVTFDIWG 130
 QY 115 QGTL 118
 DB 131 QGTM 134
 RESULT 13
 Q6MZV7 PRELIMINARY; PRT; 473 AA.

AC Q6MZV7;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686C11235;
 GN Name=DKFZp686C11235;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Human small intestine;
 RG The German Human cDNA Consortium;
 RA Boecker H., Boecker M., Meves H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wilmann S.,
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640853; CAB45920.1; -
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-sect; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00407; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 52121 MW; 9476EAE4C0BFC447 CRC64;
 Query Match 61.5%; Score 402.5; DB 2; Length 473;
 Best Local Similarity 65.6%; Pred. No. 7.3e-34;
 Matches 80; Conservative 16; Mismatches 19; Indels 7; Gaps 4;
 QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYPFTNGMHWROAPGKGLIEWGINTYGEPT 60
 DB 20 EIQLVESGGGLVQPGGSLRLSCAAGFTFSFGKHWROAPGKGLIEWLSYI-TSGNTIV 78
 QY 61 AAD-FKRFPTSLDTSKSTAYLQNNLSLAEDTAVYCAKPHYYSRHW- - - - -EDVWG 116
 DB 79 YADSLQGRFTISRDNSKNTLYLQNNLSLAEDTAVYCAKQNEH-TSPWYVSFDYWGQ 136
 QY 117 TL 118
 DB 137 IL 138
 RESULT 14
 HV23_MOUSE STANDARD; PRT; 123 AA.
 ID HV23_MOUSE
 AC P01792;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V region HPC8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE.
 RP MEDLINE=81197602; PubMed=7231520;
 RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.,
 RT "IgG antibodies to phosphorylcholine exhibit more diversity than their
 RT IGM counterparts."
 RL Nature 291:29-34 (1981).
 CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein that
 CC binds phosphorylcholine.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; E93256; AVMSH8.

DR HSSP; P01789; IMCP.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 DR Direct protein sequencing; Hybridoma; Immunoglobulin V region.
 FT DOMAIN 1 114
 FT NON_TER 123 123
 SQ SEQUENCE 123 AA; 13879 MW; 4559D3106CAF7D8D CRC64;

Query Match 61.4%; Score 402; DB 1; Length 123;
 Best Local Similarity 65.3%; Pred. No. 1.8e-34;
 Matches 79; Conservative 12; Mismatches 22; Indels 8; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGTFITNYGMWVRQAPGKGLEWVGWINT---YTG 56
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGTFITNYGMWVRQAPGKGLEWVGWINT---YTG 60

QY 57 EPTVAADFQRFTSLTSTKSTAYLQNSLRAPDTAVYYCAKPHYGSSHWYFDVWGOG 116
 DB 61 E--YSAVKGRFTVSRDTSQSLVYLQNALRAEDTAIYYCAR--DYGSRIWYFDVWGAG 116

QY 117 T 117
 DB 117 T 117

RESULT 15

Q9HCCI PRELIMINARY; PRT; 112 AA.

AC Q9HCCI;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Single chain Fv (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.,
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB049915; BAB16829.1; -.
 DR HSSP; P01789; IIGC.
 DR InterPro; IPR007110; IG-like.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 61.3%; Score 401.5; DB 2; Length 112;
 Best Local Similarity 66.1%; Pred. No. 1.9e-34;
 Matches 78; Conservative 11; Mismatches 22; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGTFITNYGMWVRQAPGKGLEWVGWINTYTGEPY 60
 DB 1 EVQLVESGGGVVAPGGSLRISCAASGTFITDYGMSWVROAPGKLEWVSGINNCGSTGY 60
 QY 61 AADFKRFTSLTSTKSTAYLQNSLRAPDTAVYYCAKPHYGSSHWYFDVWGOGTL 118
 DB 61 ADSVKGRFTISRDAKNSLYLQNSLRAPDTAVYYCAR-----RRYADYWGOGTL 111

Search completed: March 14, 2005, 20:49:18
 Job time : 84.807 secs

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OM protein - protein search, using SW model

Run on: March 14, 2005, 20:21:17 ; Search time 88.0482 Seconds
(without alignments)
483.186 Million cell updates/sec

Title: US-09-723-752B-8

Perfect score: 576

Sequence: 1 DIQMTQSPSSLSASVGRVT.....YSTVPTFGQCTKVEIKRTV 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	576	100.0	110	3	AAB05897 Humanised
2	576	100.0	110	3	AAB13376 F(ab)-12
3	576	100.0	237	8	ADQ90721 Anti-VEGF
4	573	99.5	110	2	AAW70677 Anti-VEGF
5	573	99.5	110	2	AAW70687 Anti-VEGF
6	573	99.5	110	3	AAB13380 Anti-VEGF
7	573	99.5	110	5	ABP61256 Humanised
8	573	99.5	110	5	ABP61246 Humanised
9	573	99.5	214	7	ADC26154 Parent an
10	573	99.5	237	5	ABB81107 Anti-VEGF
11	573	99.5	237	5	ABP51952 Plasmid P
12	573	99.5	237	8	ADQ14128 Plasmid P
13	573	99.5	237	8	ADQ14131 Plasmid P
14	573	99.5	237	8	ADQ90703 Anti-VEGF
15	573	99.5	237	8	ADQ90701 Anti-VEGF
16	573	99.5	237	8	ADQ90705 Anti-VEGF
17	573	99.5	237	8	ADQ90709 Anti-VEGF
18	573	99.5	237	8	ADQ90723 Anti-VEGF
19	573	99.5	237	8	ADQ90707 Anti-VEGF
20	570	99.0	110	2	AAW70675 Anti-VEGF
21	570	99.0	110	5	ABP61244 Humanised
22	567	98.4	108	5	AAW70618 Humanised
23	567	98.4	108	5	ABP61187 Humanised
24	567	98.4	108	8	ADG31782 V(L) doma
25	567	98.4	108	8	ADG31768 V(L) doma

26	567	98.4	108	8	ADG31893	ADG31893 V(L) prot
27	567	98.4	110	2	AAW70673	AAW70673 Anti-VEGF
28	567	98.4	110	5	ABP61242	ABP61242 Humanised
29	567	98.4	237	2	AAW70703	AAW70703 Protein e
30	567	98.4	650	5	ABP61241	ABP61241 Phage-dls
31	564	97.9	108	8	ADG31770	ADG31770 V(L) doma
32	561	97.4	108	2	AAW70696	AAW70696 Anti-VEGF
33	561	97.4	108	5	ABP61265	ABP61265 Humanised
34	559	97.0	107	2	AAW70683	AAW70683 Variable
35	559	97.0	107	2	AAW70623	AAW70623 Humanised
36	559	97.0	107	5	ABP61192	ABP61192 Humanised
37	556	96.5	107	2	AAW86805	AAW86805 Variable
38	556	96.5	107	2	AAW70625	AAW70625 Humanised
39	556	96.5	107	2	AAW61194	AAW61194 Humanised
40	556	96.5	214	7	ADC26157	ADC26157 Anti-VEGF
41	555	96.4	214	7	ADC26156	ADC26156 Anti-VEGF
42	554	96.2	110	2	AAW70685	AAW70685 Anti-VEGF
43	554	96.2	110	2	AAW70681	AAW70681 Anti-VEGF
44	554	96.2	110	2	AAW70683	AAW70683 Anti-VEGF
45	554	96.2	110	2	AAW70679	AAW70679 Anti-VEGF

ALIGNMENTS

RESULT 1	
AAB05897	standard; peptide; 110 AA.
ID	AAB05897
AC	AAB05897;
DT	17-OCT-2000 (first entry)
XX	
DE	Humanised anti-VEGF antibody F(ab)-12 light chain variable domain.
XX	
KW	Humanised, F(ab)-12, light chain variable domain; antibody variant;
KW	phage display; randomised library; cytosolic; antiarteriosclerotic;
KW	antipneumatic; antidiabetic; antiinflammatory; antiarteriosclerotic;
KW	vascular endothelial growth factor; VEGF; breast cancer; lung cancer;
KW	retinoblastoma; rheumatoid arthritis; psoriasis; atherosclerosis;
KW	diabetic retinopathy; complementarily determining region; CDR.
XX	
OS	Homo sapiens.
XX	
XX	Synthetic.
XX	
XX	WO200029584-A1.
XX	
XX	25-MAY-2000.
XX	
XX	16-NOV-1999; 99WC-US027153.
XX	
XX	FR 18-NOV-1998; 98US-0108945P.
XX	
XX	(GETH) GENENTECH INC.
PI	Chen YM, Lowman HB, Muller Y;
XX	
XX	WPI, 2000-387797/33.
XX	
XX	Antibody variants with higher binding affinity than native antibodies
XX	useful for diagnosis, prevention and treatment of neoplastic and non-
PT	neoplastic diseases comprises amino acid insertion in hypervariable
PT	region.
XX	
XX	Disclosure; Fig 1A; 110p; English.
PS	
XX	
CC	The present sequence is the light chain variable domain of F(ab)-12, a
CC	humanised anti-vascular endothelial growth factor (VEGF) antibody. F(ab)-
CC	12 was the parent antibody used in the production of a large number of
CC	antibody variants containing randomised peptide inserts within the
CC	complementarily determining regions (CDRs). Phage display libraries were
CC	subjected to eight rounds of selection to isolate variants with an
CC	antigen binding affinity at least two-fold stronger than the binding

CC affinity of parent antibody for the target VEGF antibody. The anti-VEGF
 CC antibody variants may be useful in diagnostic assays for detecting
 CC expression of VEGF in cells, tissue or serum. They may also be used in
 CC the prevention and treatment of neoplastic diseases such as breast
 CC cancer, lung cancer and retinoblastoma, and non-neoplastic diseases
 CC including rheumatoid arthritis, psoriasis, atherosclerosis, and diabetic
 CC and other proliferative retinopathies

XX Sequence 110 AA:

Query Match 100.0%; Score 576; DB 3; Length 110;
 Best Local Similarity 100.0%; Pred. No. 7.5e-33;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQKPKAKVLIYFTSSLSHGVPS 60
 DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQKPKAKVLIYFTSSLSHGVPS 60
 QY 61 RFSGSGSGTDFTLTISLSLOPEDPATYCCQYSTVPMTFGGGTVEIKRTV 110
 DB 61 RFSGSGSGTDFTLTISLSLOPEDPATYCCQYSTVPMTFGGGTVEIKRTV 110

RESULT 2

ID AAB13376 standard; protein; 110 AA.

XX AAB13376;

DT 12-SEP-2003 (revised)
 DT 21-NOV-2000 (first entry)

DE F(ab)-12 anti-VEGF antibody light chain variable domain.

XX Humanised; F(ab)-12; vascular endothelial cell growth factor; VEGF;
 KM antibody; antiinflammatory; cerebroprotective; cyostatic; antirheumatic;
 KM antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic;
 KM antihydroid; excessive neovascularisation; tumour; rheumatoid arthritis;
 KM psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
 KM neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
 KM tissue transplantation; inflammation; oedema; trauma;
 KM complementarity determining region; CDR.

OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.

XX Key Location/Qualifiers

FT Region 24..34 /label= CDR-L1
 FT Region 50..56 /label= CDR-L2
 FT Region 89..97 /label= CDR-L3

XX MO200037502-A2.

XX 29-JUN-2000.

XX 09-DEC-1999; 99MO-US029475.

XX 22-DEC-1998; 98US-00218481.

XX (GETH) GENENTECH INC.

XX Van Bruggen N; Ferrara N;

XX WPI; 2000-442646/38.

PT Treating edema, tumor, rheumatoid arthritis, psoriasis, atherosclerosis,
 PT diabetes and chronic inflammation in a mammal, comprises administering a
 PT human vascular endothelial cell growth factor antagonist.

PS Disclosure; Fig 1A; 60pp; English.

XX The present sequence is the light chain variable domain of humanised anti-
 CC -vascular endothelial cell growth factor (anti-VEGF) antibody F(ab)-12.
 CC It may be used to treat conditions characterised by undesirable excessive
 CC neovascularisation. Such conditions include tumours (especially solid
 CC ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
 CC other retinopathies, retrolental fibroplasia, age-related macular
 CC degeneration, neovascular glaucoma, haemangioma, thyroid hyperplasia
 CC (including Grave's disease), corneal and other tissue transplantation,
 CC and chronic inflammation. Oedemas associated with tumours, strokes and
 CC head trauma, and ascites associated with malignancies, myel's syndrome,
 CC lung inflammation, nephrotic syndrome, pericardial effusion and pleural
 CC effusion, may also be treated. Affinity matured anti-VEGF antibodies are
 CC also used as therapeutic agents. Monoclonal antibodies are generated in
 CC hybridoma cells and those with affinity for VEGF are identified by 12-SEP-
 CC immunoprecipitation or by an in vitro binding assay. (Updated on 12-SEP-
 CC 2003 to standardise OS field)

XX Sequence 110 AA:

Query Match 100.0%; Score 576; DB 3; Length 110;
 Best Local Similarity 100.0%; Pred. No. 7.5e-33;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQKPKAKVLIYFTSSLSHGVPS 60
 DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQKPKAKVLIYFTSSLSHGVPS 60
 QY 61 RFSGSGSGTDFTLTISLSLOPEDPATYCCQYSTVPMTFGGGTVEIKRTV 110
 DB 61 RFSGSGSGTDFTLTISLSLOPEDPATYCCQYSTVPMTFGGGTVEIKRTV 110

RESULT 3

ID ADQ90721 standard; protein; 237 AA.

XX ADQ90721;

DT 21-OCT-2004 (first entry)

DE Anti-VEGF antibody light chain protein SEQ ID NO:25.

XX antibody; antigen binding fragment; cell culture; variable domain;
 KM modified framework region; hypervariable region; cyostatic;
 KM antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 KM tumour; inflammatory disorder; angiogenic disorder;
 KM immunological disorder; anti-VEGF antibody;
 KM anti vascular endothelial cell growth factor antibody; light chain.

OS Homo sapiens.
 OS Synthetic.

XX MO2004065417-A2.

XX 05-AUG-2004.

XX 23-JAN-2004; 2004MO-US001844.

XX 23-JAN-2003; 2003US-0442484P.

XX (GETH) GENENTECH INC.

XX Simmons L;

XX WPI; 2004-562149/54.

XX N-PSDB; ADQ90720.

PT Producing an antibody or antigen binding fragment in high yield in a cell
 PT culture, comprises expressing a variable domain with a modified framework
 PT region in a host cell.

PS Example 6, SEQ ID NO 25, 161pp; English.

CC The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding
 CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC (VH1) and/or VH2 amino acid sequence that has a hypervariable region 1
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents the light chain of an anti-VEGF (vascular endothelial
 CC cell growth factor) antibody, which is used in the exemplification of the
 CC present invention.

XX Sequence 237 AA;

Query Match 100.0%; Score 576; DB 8; Length 237;

Best Local Similarity 100.0%; Pred. No. 1.5e-32; Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGRVITTCASQDINSYLNMYQKPKAPKVLITYFTSSLSHGVP 60
 Db 24 DIQMTSPSSLSASVGRVITTCASQDINSYLNMYQKPKAPKVLITYFTSSLSHGVP 83
 Qy 61 RFSGSGSGTDFLTITSSLOPEDPATYCCQYSTVPMTFGGKTVEIKRTV 110
 Db 84 RFSGSGSGTDFLTITSSLOPEDPATYCCQYSTVPMTFGGKTVEIKRTV 133

RESULT 4

AAW70677 ID AAW70677 standard; peptide; 110 AA.

XX AAW70677;

XX 27-JAN-1999 (first entry)

XX Anti-VEGF humanised antibody variable light domain of variant Y0101.

XX Light variable domain; murine; humanised antibody;

XX anti-vascular endothelial growth factor antibody; anti-VEGF antibody;

XX VEGF-induced angiogenesis; tumour; retinal disorder;

XX age-related macular degeneration; diabetic retinopathy;

XX rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

XX Synthetic.

XX Mus sp.

XX Homo sapiens.

XX WO9845331-A2.

XX 15-OCT-1998.

XX 03-APR-1998; 98MO-US006604.

XX 07-APR-1997; 97US-00833504.

XX 06-AUG-1997; 97US-00908469.

PA (GETH) GENENTECH INC.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI; 1998-568337/48.

XX New humanised antibody with affinity for vascular endothelial growth

XX factor - for treatment of tumours, retinal disease and other angiogenic

XX PT states, also related nucleic acid, vectors and transformed cells.

XX Example 3; Fig 9A; 100pp; English.

XX The present sequence represents a variable light domain of an affinity-
 CC matured anti-vascular endothelial growth factor (anti-VEGF) antibody
 CC variant. The sequence is used in the course of the invention to produce
 CC the humanised anti-VEGF antibody of the invention. The humanised
 CC antibodies are used to inhibit VEGF-induced angiogenesis, particularly
 CC for treating or preventing tumours (of any type) and retinal disorders
 CC (e.g. age-related macular degeneration or diabetic retinopathy). They can
 CC also be used to treat other conditions that involve angiogenesis, e.g.
 CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc

XX Sequence 110 AA;

Query Match 99.5%; Score 573; DB 2; Length 110;

Best Local Similarity 99.1%; Pred. No. 1.2e-32; Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGRVITTCASQDINSYLNMYQKPKAPKVLITYFTSSLSHGVP 60
 Db 1 DIQMTSPSSLSASVGRVITTCASQDINSYLNMYQKPKAPKVLITYFTSSLSHGVP 60
 Qy 61 RFSGSGSGTDFLTITSSLOPEDPATYCCQYSTVPMTFGGKTVEIKRTV 110
 Db 61 RFSGSGSGTDFLTITSSLOPEDPATYCCQYSTVPMTFGGKTVEIKRTV 110

RESULT 5

AAW70687 ID AAW70687 standard; peptide; 110 AA.

XX AAW70687;

XX 27-JAN-1999 (first entry)

XX Anti-VEGF humanised antibody variable light domain of variant Y0317.

XX Light variable domain; murine; humanised antibody;

XX anti-vascular endothelial growth factor antibody; anti-VEGF antibody;

XX VEGF-induced angiogenesis; tumour; retinal disorder;

XX age-related macular degeneration; diabetic retinopathy;

XX rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

XX Synthetic.

XX Mus sp.

XX Homo sapiens.

XX WO9845331-A2.

XX 15-OCT-1998.

XX 03-APR-1998; 98MO-US006604.

XX 07-APR-1997; 97US-00833504.

XX 06-AUG-1997; 97US-00908469.

XX (GETH) GENENTECH INC.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI; 1998-568337/48.

XX New humanised antibody with affinity for vascular endothelial growth

factor - for treatment of tumours, retinal disease and other angiogenic states, also related nucleic acid, vectors and transformed cells.

Claim 27; Fig 10A; 100pp; English.

XX The present sequence represents a variable light domain of an affinity-matured anti-vascular endothelial growth factor (anti-VEGF) antibody variant. The sequence is used in the course of the invention to produce the humanised anti-VEGF antibody of the invention. The humanised antibodies are used to inhibit VEGF-induced angiogenesis, particularly for treating or preventing tumours (of any type) and retinal disorders (e.g. age-related macular degeneration or diabetic retinopathy). They can also be used to treat other conditions that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc

SO Sequence 110 AA;
Query Match 99.5%; Score 573; DB 2; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.2e-32;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Dy 1 DIQWTPSSLSASVGVDRVTITCSASODISNYLWYQOKPGKAPKVLITYFTSSLSHGVS 60
1 DIQWTPSSLSASVGVDRVTITCSASODISNYLWYQOKPGKAPKVLITYFTSSLSHGVS 60

Qy 61 RFSGSGSGTDFTLTITSLQPEDFATYYCQYSTVPMWFGGTGKVEIKRTV 110
61 RFSGSGSGTDFTLTITSLQPEDFATYYCQYSTVPMWFGGTGKVEIKRTV 110

Db 61 RFSGSGSGTDFTLTITSLQPEDFATYYCQYSTVPMWFGGTGKVEIKRTV 110

RESULT 6
AAB13380 ID AAB13380 standard; protein; 110 AA.
XX AAB13380;
XX 21-NOV-2000 (first entry)

XX Anti-VEGF antibody Y0317 light chain variable domain.

XX Y0317; vascular endothelial cell growth factor; VEGF; antibody;
XX antiinflammatory; cerebroprotective; cytoprotective; antirheumatic;
XX antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic;
XX antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
XX psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
XX neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
XX tissue transplantation; inflammation; oedema; trauma;
XX complementarity determining region; CDR.

XX Unidentified.

XX Key Location/Qualifiers
XX Region 24..33 /label= CDR-L1
XX Region 50..56 /label= CDR-L2
XX Region 89..97 /label= CDR-L3

XX WO200037502-A2.
XX 29-JUN-2000.

XX 09-DEC-1999; 99WO-US029475.

XX 22-DEC-1998; 98US-00218481.

XX (GETH) GENENTECH INC.

XX Van Bruggen N, Ferrara N;

XX WPI, 2000-442646/38.

PT Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and chronic inflammation in a mammal, comprises administering a human vascular endothelial cell growth factor antagonist.

XX Disclosure; Fig 14A; 60pp; English.

XX The present sequence is the light chain variable region of the affinity-matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody Y0317. Humanised Fab-12 and affinity matured anti-VEGF antibodies may be used to treat conditions characterised by undesirable excessive neovascularisation. Such conditions include tumours (especially solid ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and other retinopathies, retrolental fibroplasia, age-related macular degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias (including Grave's disease), corneal and other tissue transplantation, and chronic inflammation. Oedemas associated with tumours, strokes and head trauma, and ascites associated with malignancies, melg's syndrome, lung inflammation, nephrotic syndrome, pericardial effusion and pleural effusion, may also be treated. Monoclonal antibodies are generated in hybridoma cells and those with affinity for VEGF are identified by immunoprecipitation or by an in vitro binding assay

SO Sequence 110 AA;
Query Match 99.5%; Score 573; DB 3; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.2e-32;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Dy 1 DIQWTPSSLSASVGVDRVTITCSASODISNYLWYQOKPGKAPKVLITYFTSSLSHGVS 60
1 DIQWTPSSLSASVGVDRVTITCSASODISNYLWYQOKPGKAPKVLITYFTSSLSHGVS 60

Qy 61 RFSGSGSGTDFTLTITSLQPEDFATYYCQYSTVPMWFGGTGKVEIKRTV 110
61 RFSGSGSGTDFTLTITSLQPEDFATYYCQYSTVPMWFGGTGKVEIKRTV 110

Db 61 RFSGSGSGTDFTLTITSLQPEDFATYYCQYSTVPMWFGGTGKVEIKRTV 110

RESULT 7
ABP61256 ID ABP61256 standard; protein; 110 AA.
XX ABP61256;
XX 20-SEP-2002 (first entry)

XX Humanised anti-VEGF Y0317 antibody variable light domain.

XX Cytoprotective; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
XX vascular endothelial growth factor; angiogenesis inhibitor; tumour;
XX retinal disorder; intraocular neovascular disorder; Y0317; light chain;
XX variable domain.

XX Homo sapiens.
XX Mus sp.
XX Synthetic.

XX Key Location/Qualifiers
XX Domain 24..34 /label= CDR-L1
XX Domain 50..56 /label= CDR-L2
XX Domain 89..97 /label= CDR-L3

XX US2002032315-A1.

XX 14-MAR-2002.

XX 06-APR-1998; 98US-00056160.

XX 06-AUG-1997; 97US-0054856P.

XX (BACA/) BACA M.

PA (WELL/) WELLS J A.
 PA (PRES/) PRESTA L G.
 PA (LOWM/) LOWMAN H B.
 PA (CHEN/) CHEN Y M.
 XX
 PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
 DR WPI; 2002-517920/55.
 XX
 PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
 PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
 PT mammal, particularly for treating tumor or retinal disorders.
 XX
 PS Claim 27; Fig 10; 47pp; English.
 XX
 CC The present invention relates to humanised anti-VEGF (vascular
 CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
 CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
 CC particularly those having a tumour or a retinal disorder e.g. intracocular
 CC neovascular disorders. The present sequence is an exemplary light chain
 CC variable domain of the humanised anti-VEGF antibody of the invention
 XX
 SQ Sequence 110 AA;

Query Match 99.5%; Score 573; DB 5; Length 110;
 Best Local Similarity 99.1%; Pred. No. 1.2e-32;
 Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIQMTSPSSLSASVGDRTVITCSASQDISNYLNMWYQOKPGKAPKVLITYFTSSLHSGVPS 60
 DB 1 DIQLTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQOKPGKAPKVLITYFTSSLHSGVPS 60
 OY 61 RFSSGSGSTDFLTLLTSSLPQEDPATYCCQYSTVPWTFGGTKVEIKRTV 110
 DB 61 RFSSGSGSTDFLTLLTSSLPQEDPATYCCQYSTVPWTFGGTKVEIKRTV 110

RESULT 8
 ABP61246
 ID ABP61246 standard; protein; 110 AA.
 AC ABP61246;
 XX
 DT 20-SEP-2002 (first entry)
 XX
 DE Humanised anti-VEGF Y0101 antibody variable light domain.
 XX
 KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
 KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
 KW retinal disorder; intracocular neovascular disorder; Y0101; light chain;
 KW variable domain.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT 24..34
 FT /label= CDR-L1
 FT 50..57
 FT /label= CDR-L2
 FT 89..97
 FT /label= CDR-L3
 XX
 XX US2002032315-A1.
 XX
 XX 14-MAR-2002.
 XX
 XX 06-APR-1998; 98US-00056160.
 XX
 XX 06-AUG-1997; 97US-0054856P.
 XX
 XX

PA (BACA/) BACA M.
 PA (WELL/) WELLS J A.
 PA (PRES/) PRESTA L G.
 PA (LOWM/) LOWMAN H B.
 PA (CHEN/) CHEN Y M.
 XX
 PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
 DR WPI; 2002-517920/55.
 XX
 PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
 PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
 PT mammal, particularly for treating tumor or retinal disorders.
 XX
 PS Example 3; Fig 9; 47pp; English.
 XX
 CC The present invention relates to humanised anti-VEGF (vascular
 CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
 CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
 CC particularly those having a tumour or a retinal disorder e.g. intracocular
 CC neovascular disorders. The present sequence is an exemplary light chain
 CC variable domain of the humanised anti-VEGF antibody of the invention
 XX
 SQ Sequence 110 AA;

Query Match 99.5%; Score 573; DB 5; Length 110;
 Best Local Similarity 99.1%; Pred. No. 1.2e-32;
 Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIQMTSPSSLSASVGDRTVITCSASQDISNYLNMWYQOKPGKAPKVLITYFTSSLHSGVPS 60
 DB 1 DIQLTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQOKPGKAPKVLITYFTSSLHSGVPS 60
 OY 61 RFSSGSGSTDFLTLLTSSLPQEDPATYCCQYSTVPWTFGGTKVEIKRTV 110
 DB 61 RFSSGSGSTDFLTLLTSSLPQEDPATYCCQYSTVPWTFGGTKVEIKRTV 110

RESULT 9
 ADC26154
 ID ADC26154 standard; protein; 214 AA.
 AC ADC26154;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Parent anti-VEGF Y0101 antibody wild-type light chain protein.
 XX
 KW antibody variant; cytostatic; cancer; parent; anti-VEGF;
 KW vascular endothelial growth factor; Y0101; light chain; wild-type.
 XX
 OS Unidentified.
 OS
 OS WO2003068801-A2.
 PN
 XX
 XX 21-AUG-2003.
 XX
 XX 11-FEB-2003; 2003WO-US004184.
 XX
 XX 11-FEB-2002; 2002US-0355895P.
 XX
 XX 10-SEP-2002; 2002US-0409685P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Lowman HB, Marvin JS;
 XX
 XX WPI; 2003-697521/66.
 XX
 XX Making an antibody variant of a parent antibody specific to an antigen by
 PT identifying a target amino acid residue within the variable domain of the
 PT parent antibody and substituting the target residue with a different
 PT amino acid residue.
 XX

XX Example 1, SEQ ID NO 1, 81pp, English.
PS The invention relates to a novel method for making an antibody variant of
XX a parent antibody specific to an antigen. This is achieved via
CC identifying a target amino acid residue within the variable domain of the
CC parent antibody and substituting the target residue with a different
CC replacement amino acid residue such that the charge complementarity
CC between the antibody and antigen is increased. The antibody variant of
CC the invention demonstrates cytotoxic activity whilst the method may be
CC useful for treating cancer. The current sequence is that of the parent
CC anti-VEGF (vascular endothelial growth factor) Y0101 antibody wild-type
CC light chain protein of the invention.
XX
SQ Sequence 214 AA;
Query Match 99.5%; Score 573; DB 7; Length 214;
Best Local Similarity 99.1%; Pred. No. 2.2e-32;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLWMYQOKPGKAPKYLIFTSLSHGVS 60
DB 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLWMYQOKPGKAPKYLIFTSLSHGVS 60
QY 61 RFGSGSGTDFLTITSSLOPEDPATYCCQYSTVPMTFGQGTKEIKRTV 110
DB 61 RFGSGSGTDFLTITSSLOPEDPATYCCQYSTVPMTFGQGTKEIKRTV 110
RESULT 10
ID ABB81107 standard; protein, 237 AA.
AC ABB81107;
XX
DT 05-NOV-2002 (first entry)
XX
DE Anti-VEGF light chain fragment.
XX
KW Immunoglobulin; promoter; cytostatic; antiinflammatory; immunomodulator;
KW neuroprotective; CD11; tissue factor; vascular endothelial growth factor;
KW VEGF.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
XX FH 1..23
XX FT /note= "STII signal sequence TIR-1"
XX FT Protein 24..237
XX FT /note= "anti-VEGF light chain"
XX
XX WO200261090-A2.
XX
XX 08-AUG-2002.
XX
XX 13-DEC-2001; 2001WO-US048691.
XX
XX 14-DEC-2000; 2000US-0256164P.
XX
XX (GETH) GENENTECH INC.
XX
XX PI Simmons LC, Klimowski L, Reilly DE, Yaneura DG;
XX
XX WPI; 2002-619253/66.
XX
XX N-PsDB; ABB86646.
XX
XX New polynucleotide comprising first and second promoter-cistron pairs,
XX useful for diagnosing, treating or preventing diseases associated with
XX abnormal expression and/or activity of antigens such as inflammatory
XX disorders.
XX
XX Disclosure; Fig 21A-C; 104pp; English.
XX

CC The invention provides a polynucleotide, which encodes an immunoglobulin
CC (Ig), comprising a first or second promoter-cistron pair consisting of a
CC first or second promoter and cistron, respectively. The first cistron of
CC the first promoter-cistron pair comprises a first translational
CC initiation region (TIR-1) operably linked to a nucleic acid sequence
CC encoding an Ig light chain and the second cistron of the second promoter-
CC cistron pair comprises a second translational initiation region (TIR-H)
CC operably linked to a nucleic acid sequence encoding an Ig heavy chain.
CC Upon expression of the polynucleotide in a prokaryotic host cell, light
CC and heavy chains are folded and assembled to form a biologically active
CC Ig. The antibody of the invention is useful for diagnosing, treating or
CC preventing diseases or conditions associated with abnormal expression and
CC /or activity of one or more antigen molecules e.g. lymphoid malignancies,
CC inflammatory, angiogenic, immunologic, neuronal, glial, astrocytal,
CC hypothalamic or other glandular disorders. The present sequence
CC represents the amino acid sequence of an anti-vascular endothelial growth
CC factor (VEGF) light chain fragment of the cistron vector pXV02ABP1
XX
SQ Sequence 237 AA;
Query Match 99.5%; Score 573; DB 5; Length 237;
Best Local Similarity 99.1%; Pred. No. 2.4e-32;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLWMYQOKPGKAPKYLIFTSLSHGVS 60
DB 24 DIQMTQSPSSLSASVGRVTITCSASQDISNYLWMYQOKPGKAPKYLIFTSLSHGVS 83
QY 61 RFGSGSGTDFLTITSSLOPEDPATYCCQYSTVPMTFGQGTKEIKRTV 110
DB 84 RFGSGSGTDFLTITSSLOPEDPATYCCQYSTVPMTFGQGTKEIKRTV 133
RESULT 11
ID ABP51952 standard; protein, 237 AA.
AC ABP51952;
XX
XX 09-OCT-2002 (first entry)
XX
XX Plasmid pX0317 anti-VEGF Fab amino acid sequence SEQ ID NO:2 #1.
XX
XX Bacterial host; protease; degP; prc; spr; anti-VEGF antibody; antibody;
XX humanised; Apo2 ligand; anti-CD18; anti-tissue factor; 2c4; anti-CD20;
XX anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;
XX anti-CD11a; Fab'; Fab'2; Fab'2-leucine zipper fusion; anti-VEGF Fab.
XX
XX Mus sp.
XX Escherichia coli.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH 1..23
XX FT /label= signal
XX FT Protein 24..237
XX FT /label= anti-VEGF_Fab
XX
XX WO200248376-A2.
XX
XX 20-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US047581.
XX
XX 14-DEC-2000; 2000US-0256162P.
XX
XX (GETH) GENENTECH INC.
XX
XX PI Chen CY;
XX
XX WPI; 2002-583522/62.
XX
XX N-PsDB; AB073919.
XX

PT Novel Escherichia coli strain useful for producing polypeptide, deficient
PT in deap and prc encoding protease, and harboring mutant spr gene, product
PT of gene suppresses growth phenotypes of strains harboring prc mutants.
XX

PS Example 1; Fig 1A-C; 63pp; English.

CC The present invention describes an Escherichia coli strain (1) deficient
CC in chromosomal deap and prc encoding protease and prc, respectively,
CC and harbouring a mutant spr gene, the product of mutant spr gene
CC suppresses growth phenotypes exhibited by strains harbouring prc mutants.
CC (1) is useful for producing a polypeptide, by culturing (1) comprising
CC nucleic acid encoding the polypeptide, which is heterologous to the
CC strain, such that the nucleic acid is expressed, and recovering the
CC heterologous polypeptide from the strain. The heterologous polypeptide is
CC proteolytically sensitive. Culturing of (1) is performed in a fermentor
CC under conditions of high- or low-cell density fermentation. The
CC polypeptide is recovered from the periplasm or culture medium of the
CC strain. The polypeptide is an antibody (humanised or full-length
CC antibody) or Ap02 ligand. The antibody is an anti-CD18, anti-vascular
CC endothelial growth factor (VEGF), anti-tissue factor, 2c4, anti-Her-2,
CC anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an
CC antibody fragment having a light chain (kappa light chain). The antibody
CC fragment is a Fab, Fab', Fab'2 or Fab'2-leucine zipper fusion, anti-CD18
CC Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper
CC fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-
CC tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, or anti-
CC Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18
CC represents an anti-VEGF Fab amino acid sequence from the present
CC invention
CC

XX Sequence 237 AA:

Query Match 99.5%; Score 573; DB 5; Length 237;
Best Local Similarity 99.1%; Pred. No. 2.4e-32;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTQSSLSASVGRVITTCASQDISNYLMWYQOKRGKAPKVIYFTSSLHSGVPS 60
DB 24 DIQWTQSSLSASVGRVITTCASQDISNYLMWYQOKRGKAPKVIYFTSSLHSGVPS 83

QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQYSTVPMWFGGCTKVEIKRTV 110
DB 84 RFSGSGSGTDFTLTISLQPEDPATYCCQYSTVPMWFGGCTKVEIKRTV 133

RESULT 12
AD014128 standard; protein; 237 AA.

XX AD014128;

DT 12-AUG-2004 (first entry)

XX Plasmid pXVG2AP11 expression cassette light chain protein SEQ ID NO:8.

KW antibody; variant heavy chain hinge region; immunocjugate; cytostatic;
KM immunosuppressive; immunotherapy; tumour; cancer; immune disorder;
KW expression cassette; plasmid pXVG2AP11; anti-VEGF light chain.

XX Synthetic.

XX WO2004042017-A2.

XX 21-MAY-2004.

XX 30-OCT-2003; 2003WO-US034610.

XX 31-OCT-2002; 2002US-0422952P.

XX (GETH) GENENTECH INC.

XX Reilly D, Yansura DG;

XX WPI; 2004-390607/36.

DR N-Psdb; AD014127.

PT New antibody comprising a variant heavy chain hinge region incapable of
PT inter-heavy chain disulfide linkage, useful for treating, preventing,
PT diagnosing, delaying or preventing a disease, e.g. tumor, cancer or
PT immune disorder.

PS Example 1; SEQ ID NO 8; 124pp; English.

CC The present invention describes an antibody comprising a variant heavy
CC chain hinge region incapable of inter-heavy chain disulfide linkage. Also
CC described: (1) an antibody lacking inter-heavy chain disulfide linkage;
CC (2) an immunocjugate comprising the antibody conjugated with a
CC heterologous moiety; (3) a composition comprising the antibody or
CC immunocjugate, and carrier; (4) an article of manufacture comprising
CC the composition in a container; (5) a polynucleotide encoding the
CC antibody or immunocjugate, or a variant immunoglobulin heavy chain
CC incapable of inter-heavy chain disulfide linkage; (6) a recombinant
CC vector for expressing the antibody or immunocjugate; (7) a host cell
CC comprising the recombinant vector; (8) expressing in a host cell an
CC antibody of interest in which at least one inter-heavy chain disulfide
CC linkage is eliminated, and recovering the antibody from the host cell;
CC (9) an aglycosylated antibody produced by the method; and (10) treating,
CC preventing, diagnosing, delaying or preventing a disease in a subject.
CC The antibody has cytostatic and immunosuppressive activities, and can be
CC used in immunotherapy. The antibody, immunocjugate and methods are
CC useful for treating, preventing, diagnosing, delaying or preventing a
CC disease, e.g. tumour, cancer or immune disorder. The present sequence
CC represents the anti-VEGF light chain from the expression cassette of
CC plasmid pXVG2AP11, which is used in the exemplification of the present
CC invention.
CC

XX Sequence 237 AA:

Query Match 99.5%; Score 573; DB 8; Length 237;
Best Local Similarity 99.1%; Pred. No. 2.4e-32;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTQSSLSASVGRVITTCASQDISNYLMWYQOKRGKAPKVIYFTSSLHSGVPS 60
DB 24 DIQWTQSSLSASVGRVITTCASQDISNYLMWYQOKRGKAPKVIYFTSSLHSGVPS 83

QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQYSTVPMWFGGCTKVEIKRTV 110
DB 84 RFSGSGSGTDFTLTISLQPEDPATYCCQYSTVPMWFGGCTKVEIKRTV 133

RESULT 13
AD014131 standard; protein; 237 AA.

XX AD014131;

DT 12-AUG-2004 (first entry)

XX Plasmid pXVG11VERK expression cassette light chain protein SEQ ID NO:11.

KW antibody; variant heavy chain hinge region; immunocjugate; cytostatic;
KM immunosuppressive; immunotherapy; tumour; cancer; immune disorder;
KW expression cassette; plasmid pXVG11VERK; anti-VEGF light chain.

XX Synthetic.

XX WO2004042017-A2.

XX 21-MAY-2004.

XX 30-OCT-2003; 2003WO-US034610.

XX 31-OCT-2002; 2002US-0422952P.

XX

PA (GETH) GENENTECH INC.
 XX
 PI Relilly D, Yansura DG;
 XX
 DR WPI: 2004-390607/36.
 DR N-PSDB; ADO14130.
 XX
 PT New antibody comprising a variant heavy chain hinge region incapable of
 PT inter-heavy chain disulfide linkage, useful for treating, preventing,
 PT diagnosing, delaying or preventing a disease, e.g. tumor, cancer or
 PT immune disorder.
 XX
 PS Example 1; SEQ ID NO 11; 124pp; English.
 XX
 CC The present invention describes an antibody comprising a variant heavy
 CC chain hinge region incapable of inter-heavy chain disulfide linkage. Also
 CC described: (1) an antibody lacking inter-heavy chain disulfide linkage;
 CC (2) an immunocjugate comprising the antibody conjugated with a
 CC heterologous moiety; (3) a composition comprising the antibody or
 CC immunocjugate, and carrier; (4) an article of manufacture comprising
 CC the composition in a container; (5) a polynucleotide encoding the
 CC antibody or immunocjugate, or a variant immunoglobulin heavy chain
 CC incapable of inter-heavy chain disulfide linkage; (6) a recombinant
 CC vector for expressing the antibody or immunocjugate; (7) a host cell
 CC comprising the recombinant vector; (8) expressing in a host cell an
 CC antibody of interest in which at least one inter-heavy chain disulfide
 CC linkage is eliminated, and recovering the antibody from the host cell;
 CC (9) an glycosylated antibody produced by the method; and (10) treating,
 CC preventing, diagnosing, delaying or preventing a disease in a subject.
 CC The antibody has cytostatic and immunosuppressive activities, and can be
 CC used in immunotherapy. The antibody, immunocjugate and methods are
 CC useful for treating, preventing, diagnosing, delaying or preventing a
 CC disease, e.g. tumor, cancer or immune disorder. The present sequence
 CC represents the anti-VEGF light chain from the expression cassette of
 CC plasmid pXVGL1VERK, which is used in the exemplification of the present
 CC invention.
 CC
 XX
 SQ Sequence 237 AA;
 Query Match 99.5%; Score 573; DB 8; Length 237;
 Best Local Similarity 99.1%; Pred. No. 2,4e-32;
 Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQWTGSPSSLSASVGRVTTTCSASODISNYLWYQKRGKAPKVLITYFTSSLSHGVPS 60
 DB 24 DIQWTGSPSSLSASVGRVTTTCSASODISNYLWYQKRGKAPKVLITYFTSSLSHGVPS 83
 QY 61 RFGSGSGGTDFLTITISLQPEDPATYTCQOYSTVPMFTGGCTVVEIKRTV 110
 DB 84 RFGSGSGGTDFLTITISLQPEDPATYTCQOYSTVPMFTGGCTVVEIKRTV 133
 RESULT 14
 ADO90703
 XX ADO90703 standard; protein: 237 AA.
 AC ADO90703;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Anti-VEGF antibody Y0317 light chain protein SEQ ID NO:7.
 XX
 KW antibody; antigen binding fragment; cell culture; variable domain;
 KW modified framework region; hypervariable region; cytosolic;
 KW antiinflammatory; angiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; light chain.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX
 PN WO2004065417-A2.

XX
 PD 05-AUG-2004.
 XX
 XX 23-JAN-2004; 2004MO-US001844.
 PF
 XX 23-JAN-2003; 2003US-0442484P.
 PR
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Simmons L;
 XX
 DR WPI: 2004-562149/54.
 DR N-PSDB; ADO90702.
 XX
 PT Producing an antibody or antigen binding fragment in high yield in a cell
 PT culture, comprises expressing a variable domain with a modified framework
 PT region in a host cell.
 XX
 PS Example 2; SEQ ID NO 7; 161pp; English.
 XX
 CC The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding
 CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, angiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents the light chain of an anti-VEGF (vascular endothelial
 CC cell growth factor) antibody, which is used in the exemplification of the
 CC present invention.
 CC
 XX
 SQ Sequence 237 AA;
 Query Match 99.5%; Score 573; DB 8; Length 237;
 Best Local Similarity 99.1%; Pred. No. 2,4e-32;
 Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQWTGSPSSLSASVGRVTTTCSASODISNYLWYQKRGKAPKVLITYFTSSLSHGVPS 60
 DB 24 DIQWTGSPSSLSASVGRVTTTCSASODISNYLWYQKRGKAPKVLITYFTSSLSHGVPS 83
 QY 61 RFGSGSGGTDFLTITISLQPEDPATYTCQOYSTVPMFTGGCTVVEIKRTV 110
 DB 84 RFGSGSGGTDFLTITISLQPEDPATYTCQOYSTVPMFTGGCTVVEIKRTV 133
 RESULT 15
 ADO90701
 XX ADO90701 standard; protein: 237 AA.
 AC ADO90701;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:5.
 XX
 KW antibody; antigen binding fragment; cell culture; variable domain;

Job time : 89.0482 secs

KW modified framework region; hypervariable region; cytosolic;
 KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; light chain.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO2004065417-A2.
 XX
 PD 05-AUG-2004.
 XX
 PD 23-JAN-2004; 2004WO-US001844.
 XX
 PF 23-JAN-2003; 2003US-0442484P.
 XX
 PR 23-JAN-2003; 2003US-0442484P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Simmons L;
 XX
 DR WPI: 2004-562149/54.
 DR N-PSDB; ADQ90700.
 XX
 PT Producing an antibody or antigen binding fragment in high yield in a cell
 PT culture, comprises expressing a variable domain with a modified framework
 PT region in a host cell.
 XX
 PS Example 2; SEQ ID NO 5; 161pp; English.
 XX
 CC The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding
 CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents the light chain of an anti-VEGF (vascular endothelial
 CC cell growth factor) antibody, which is used in the exemplification of the
 CC present invention.
 CC
 XX
 SQ Sequence 237 AA;

Query Match 99.5%; Score 573; DB 8; Length 237;
 Best Local Similarity 99.1%; Pred. No. 2,4e-32;
 Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIOMTQSSSSLSASVGDRTTTCSSASODISNTLNTYQOKPGKAPKLYTFTSSLSHGVPVS 60
 DB 24 DIQLOSPSSSSLSASVGDRTTTCSSASODISNTLNTYQOKPGKAPKLYTFTSSLSHGVPVS 83
 QY 61 RPSGSGSGTDFTLTITSLQPEDFATYCCQYSTVPWTFGQGTKEIKRTV 110
 DB 84 RPSGSGSGTDFTLTITSLQPEDFATYCCQYSTVPWTFGQGTKEIKRTV 133

Search completed: March 14, 2005, 20:39:16

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 14, 2005, 20:30:13 ; Search time 22.6754 Seconds
(without alignments)
362.127 Million cell updates/sec

Title: US-09-723-752b-8

Perfect score: 576
Sequence: 1 DIQMTSPSSLSASVGDRTV.....YSTVPTFGGTVEIKRTV 110

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	576	100.0	110	4 US-09-440-781-94	Sequence 94, Appl
2	567	98.4	491	4 US-10-011-125A-2	Sequence 2, Appl
3	554	96.2	110	4 US-09-440-781-95	Sequence 95, Appl
4	525	91.1	214	2 US-07-934-373C-40	Sequence 40, Appl
5	525	91.1	214	2 US-08-788-800-11	Sequence 11, Appl
6	525	91.1	214	3 US-08-437-642B-40	Sequence 40, Appl
7	525	91.1	214	3 US-09-097-309-2	Sequence 2, Appl
8	525	91.1	214	3 US-09-097-171A-2	Sequence 2, Appl
9	525	91.1	214	3 US-09-460-587-2	Sequence 2, Appl
10	525	91.1	214	4 US-09-940-166A-2	Sequence 2, Appl
11	525	91.1	214	5 PCT-US93-07832-40	Sequence 40, Appl
12	525	91.1	233	3 US-07-934-373C-25	Sequence 25, Appl
13	525	91.1	233	3 US-08-437-642B-25	Sequence 25, Appl
14	525	91.1	233	4 US-08-146-206C-25	Sequence 25, Appl
15	525	91.1	233	4 US-09-705-686-25	Sequence 25, Appl
16	525	91.1	233	4 US-09-705-392A-25	Sequence 25, Appl
17	525	91.1	233	4 US-09-705-398-25	Sequence 25, Appl
18	525	91.1	233	5 PCT-US93-07832-25	Sequence 25, Appl
19	525	91.1	237	3 US-09-097-309-6	Sequence 6, Appl
20	525	91.1	237	3 US-09-097-171A-10	Sequence 10, Appl
21	525	91.1	237	3 US-09-432-712B-2	Sequence 2, Appl
22	525	91.1	237	3 US-09-607-756-2	Sequence 2, Appl
23	525	91.1	237	3 US-09-460-587-6	Sequence 6, Appl
24	525	91.1	237	4 US-09-940-166A-6	Sequence 6, Appl
25	522	90.6	214	1 US-08-458-516-12	Sequence 12, Appl
26	521	90.5	109	2 US-07-934-373C-47	Sequence 47, Appl
27	521	90.5	109	3 US-08-437-642B-47	Sequence 47, Appl

ALIGNMENTS

28	517	89.8	214	2 US-07-934-373C-39	Sequence 39, Appl
29	517	89.8	214	3 PCT-US93-07832-39	Sequence 39, Appl
30	517	89.8	214	5 PCT-US93-07832-39	Sequence 39, Appl
31	514	89.2	107	2 US-07-934-373C-17	Sequence 17, Appl
32	514	89.2	107	3 US-08-437-642B-17	Sequence 17, Appl
33	514	89.2	107	4 US-08-146-206C-17	Sequence 17, Appl
34	514	89.2	107	4 US-09-705-686-17	Sequence 17, Appl
35	514	89.2	107	4 US-09-705-392A-17	Sequence 17, Appl
36	514	89.2	107	4 US-09-705-398-17	Sequence 17, Appl
37	514	89.2	107	5 PCT-US93-07832-17	Sequence 17, Appl
38	514	89.2	108	3 US-08-974-899-3	Sequence 3, Appl
39	514	89.2	108	4 US-09-795-798-3	Sequence 3, Appl
40	514	89.2	127	3 US-08-649-100-33	Sequence 33, Appl
41	510	88.5	109	2 US-07-934-373C-3	Sequence 3, Appl
42	510	88.5	109	3 US-08-437-642B-3	Sequence 3, Appl
43	510	88.5	109	4 US-08-146-206C-3	Sequence 3, Appl
44	510	88.5	109	4 US-09-705-686-3	Sequence 3, Appl
45	510	88.5	109	4 US-09-705-392A-3	Sequence 3, Appl

RESULT 1
US-09-440-781-94
Sequence 94, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 94
LENGTH: 110
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-110
OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-94

Query Match 100.0%; Score 576; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLWYQKRGKAPKVLIVFTSSLHSGVPS 60
DB 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLWYQKRGKAPKVLIVFTSSLHSGVPS 60
QY 61 RFGSSGSGDFTLTISLQPEDFATYCCOYSTVPTFGGTVEIKRTV 110
DB 61 RFGSSGSGDFTLTISLQPEDFATYCCOYSTVPTFGGTVEIKRTV 110
RESULT 2
US-10-011-125A-2
Sequence 2, Application US/1001125A
Patent No. 6828121
GENERAL INFORMATION:
APPLICANT: Chen, Christina Yu-Ching
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1804R1
CURRENT APPLICATION NUMBER: US/10/011,125A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 2
LENGTH: 491
TYPE: PRT

ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Sequence is synthesized.
 Patent No. 6828121
 US-10-011-125A-2

Query Match 98.4%; Score 567; DB 4; Length 491;
 Best Local Similarity 97.3%; Pred. No. 1.1e-45;
 Matches 107; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVTITCSASQDISNYLWYQKPKKLYFTSSLSHGVPS 60
 DB 24 DIQMTSPSSLSASVGRVTITCSASQDISNYLWYQKPKKLYFTSSLSHGVPS 83
 QY 61 RFGSGSGTDTLTITSSLOPEDFATYCCQYSTVPMFGQTKVEIKRTV 110
 DB 84 RFGSGSGTDTLTITSSLOPEDFATYCCQYSTVPMFGQTKVEIKRTV 133

RESULT 3
 US-09-440-781-95
 Sequence 95; Application US/09440781
 Patent No. 6632926
 GENERAL INFORMATION:
 APPLICANT: Yvonne Man-yea Chen et al.
 TITLE OF INVENTION: ANTIBODY VARIANTS
 FILE REFERENCE: P1469R1
 CURRENT APPLICATION NUMBER: US/09/440,781
 CURRENT FILING DATE: 1999-11-16
 NUMBER OF SEQ ID NOS: 99
 SEQ ID NO 95
 LENGTH: 110
 TYPE: PRT
 ORGANISM: artificial sequence
 FEATURE:
 NAME/KEY: artificial
 LOCATION: 1-110
 OTHER INFORMATION: humanized antibody light chain variable domain
 US-09-440-781-95

Query Match 96.2%; Score 554; DB 4; Length 110;
 Best Local Similarity 94.5%; Pred. No. 3.4e-45;
 Matches 104; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVTITCSASQDISNYLWYQKPKKLYFTSSLSHGVPS 60
 DB 1 DIQMTSPSSLSASVGRVTITCSASQDISNYLWYQKPKKLYFTSSLSHGVPS 60
 QY 61 RFGSGSGTDTLTITSSLOPEDFATYCCQYSTVPMFGQTKVEIKRTV 110
 DB 61 RFGSGSGTDTLTITSSLOPEDFATYCCQYSTVPMFGQTKVEIKRTV 110

RESULT 4
 US-07-934-373C-40
 Sequence 40; Application US/07934373C
 Patent No. 5821337
 GENERAL INFORMATION:
 APPLICANT: Paul J. Carter
 APPLICANT: Leonard G. Presta
 TITLE OF INVENTION: Immunoglobulin Variants
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/934,373C
 FILING DATE: 21-Aug-1992
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/05126
 FILING DATE: 15-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0709P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 214 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-07-934-373C-40

Query Match 91.1%; Score 525; DB 2; Length 214;
 Best Local Similarity 90.9%; Pred. No. 3.9e-42;
 Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVTITCSASQDISNYLWYQKPKKLYFTSSLSHGVPS 60
 DB 1 DIQMTSPSSLSASVGRVTITCSASQDISNYLWYQKPKKLYFTSSLSHGVPS 60
 QY 61 RFGSGSGTDTLTITSSLOPEDFATYCCQYSTVPMFGQTKVEIKRTV 110
 DB 61 RFGSGSGTDTLTITSSLOPEDFATYCCQYSTVPMFGQTKVEIKRTV 110

RESULT 5
 US-08-788-800-11
 Sequence 11; Application US/08788800
 Patent No. 5914112
 GENERAL INFORMATION:
 APPLICANT: Bednar, Martin M.
 APPLICANT: Thomas, G. Roger
 APPLICANT: Gross, Cordell E.
 TITLE OF INVENTION: Anti-CD18 ANTIBODIES IN STROKE
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/788,800
 FILING DATE: 22-Jan-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0987t1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1994
 TELEFAX: 415/952-9881
 TELEEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-788-800-11

Query Match 91.1%; Score 525; DB 2; Length 214;
Best Local Similarity 90.9%; Pred. No. 3.9e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLWYQKPKAPKVLITFTSLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQDINNLYWYQKPKAPKVLITFTSLHSGVPS 60
QY 61 RFSGSGSGTDFTLTITSLQPEDFATYYCOQXSTVPWTFGGGTKEIKRTV 110
DB 61 RFSGSGSGTDYTLTITSLQPEDFATYYCOQGNLTPPTFGGTKEIKRTV 110

RESULT 6

US-08-437-642B-40
Sequence 40, Application US/08437642B
Patent No. 6054237

GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-MAY-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-437-642B-40

Query Match 91.1%; Score 525; DB 3; Length 214;
Best Local Similarity 90.9%; Pred. No. 3.9e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLWYQKPKAPKVLITFTSLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQDINNLYWYQKPKAPKVLITFTSLHSGVPS 60

QY 61 RFSGSGSGTDFTLTITSLQPEDFATYYCOQXSTVPWTFGGGTKEIKRTV 110
DB 61 RFSGSGSGTDYTLTITSLQPEDFATYYCOQGNLTPPTFGGTKEIKRTV 110

RESULT 7

US-09-097-309-2
Sequence 2, Application US/09097309
Patent No. 6121428

GENERAL INFORMATION:
APPLICANT: Blank, Gregory S.
APPLICANT: Nandirey, Daljit S.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,309
FILING DATE: 12-JUN-1998
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050951
FILING DATE: 13-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-09-097-309-2

Query Match 91.1%; Score 525; DB 3; Length 214;
Best Local Similarity 90.9%; Pred. No. 3.9e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLWYQKPKAPKVLITFTSLHSGVPS 60

DB 1 DIQMTQSPSSLSASVGRVTITCRASQDINNLYWYQKPKAPKVLITFTSLHSGVPS 60

QY 61 RFSGSGSGTDFTLTITSLQPEDFATYYCOQXSTVPWTFGGGTKEIKRTV 110

DB 61 RFSGSGSGTDYTLTITSLQPEDFATYYCOQGNLTPPTFGGTKEIKRTV 110

RESULT 8

US-09-097-171A-2
Sequence 2, Application US/09097171A
Patent No. 6171586

GENERAL INFORMATION:
APPLICANT: Lam, Xanthé M.
APPLICANT: Oeswein, James Q.

Query Match 91.1%; Score 525; DB 3; Length 214;
Best Local Similarity 90.9%; Pred. No. 3.9e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

APPLICANT: Ongpibatnanakul, Boonari
APPLICANT: Shahrokh, Zahra
APPLICANT: Wang, Sharon X.
APPLICANT: Weissburg, Robert P.
APPLICANT: Wong, Rita L.
TITLE OF INVENTION: Antibody Formulation
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,171A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/874897
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1089R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/425-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-097-171A-2

Query Match 91.1%; Score 525; DB 3; Length 214;
Best Local Similarity 90.9%; Pred. No. 3.9e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDRTTITCSASODISNTNLTMYQQRPGKAPKLLIYFTSLHSGVGS 60
DB 1 DIQMTQSPSSLSASVDRTTITCRASQDINNLTMYQQRPGKAPKLLIYFTSLHSGVGS 60
QY 61 RSSGSGSDTFTLTISLQPEDPATYTCQOYSTVPWTFGGGTVEIKRTV 110
DB 61 RSSGSGSDTFTLTISLQPEDPATYTCQOQNTLPPTFGGTVEIKRTV 110

RESULT 9
US-09-460-587-2
Sequence 2, Application US/09460587
Patent No. 6322997
GENERAL INFORMATION:
APPLICANT: Blank, Gregory S.
APPLICANT: Narindray, Daljit S.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460,587
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/097,309
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-460-587-2

Query Match 91.1%; Score 525; DB 3; Length 214;
Best Local Similarity 90.9%; Pred. No. 3.9e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDRTTITCSASODISNTNLTMYQQRPGKAPKLLIYFTSLHSGVGS 60
DB 1 DIQMTQSPSSLSASVDRTTITCRASQDINNLTMYQQRPGKAPKLLIYFTSLHSGVGS 60
QY 61 RSSGSGSDTFTLTISLQPEDPATYTCQOYSTVPWTFGGGTVEIKRTV 110
DB 61 RSSGSGSDTFTLTISLQPEDPATYTCQOQNTLPPTFGGTVEIKRTV 110

RESULT 10
US-09-940-166A-2
Sequence 2, Application US/09940166A
Patent No. 6716598
GENERAL INFORMATION:
APPLICANT: Blank, Gregory S.
APPLICANT: Narindray, Daljit S.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/940,166A
FILING DATE: 27-AUG-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/097,309
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-09-940-166A-2

Query Match 91.1%; Score 525; DB 4; Length 214;
Best Local Similarity 90.9%; Pred. No. 3.9e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDRTVITTCASQDISNYLNWYQOKPKAKPKLIYTTSLHSGVPS 60
1 DIQWTQSPSSLSASVGDRTVITTCASQDISNYLNWYQOKPKAKPKLIYTTSLHSGVPS 60
DB 1 DIQWTQSPSSLSASVGDRTVITTCASQDISNYLNWYQOKPKAKPKLIYTTSLHSGVPS 60
61 RFSGSGSGDTYTLTISLSLOPEDPATYTCQOQNTLPTFGGKTVEIKRTV 110
61 RFSGSGSGDTYTLTISLSLOPEDPATYTCQOQNTLPTFGGKTVEIKRTV 110

RESULT 11
PCT-US93-07832-40
Sequence 40, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Pointe San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-07832-40

Query Match 91.1%; Score 525; DB 5; Length 214;
Best Local Similarity 90.9%; Pred. No. 3.9e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIQWTQSPSSLSASVGDRTVITTCASQDISNYLNWYQOKPKAKPKLIYTTSLHSGVPS 60
1 DIQWTQSPSSLSASVGDRTVITTCASQDISNYLNWYQOKPKAKPKLIYTTSLHSGVPS 60

DB 1 DIQWTQSPSSLSASVGDRTVITTCASQDISNYLNWYQOKPKAKPKLIYTTSLHSGVPS 60
QY 61 RFSGSGSGDTYTLTISLSLOPEDPATYTCQOQNTLPTFGGKTVEIKRTV 110
61 RFSGSGSGDTYTLTISLSLOPEDPATYTCQOQNTLPTFGGKTVEIKRTV 110
DB 61 RFSGSGSGDTYTLTISLSLOPEDPATYTCQOQNTLPTFGGKTVEIKRTV 110

RESULT 12
US-07-934-373C-25
Sequence 25, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-07-934-373C-25

Query Match 91.1%; Score 525; DB 2; Length 233;
Best Local Similarity 90.9%; Pred. No. 4.3e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDRTVITTCASQDISNYLNWYQOKPKAKPKLIYTTSLHSGVPS 60
1 DIQWTQSPSSLSASVGDRTVITTCASQDISNYLNWYQOKPKAKPKLIYTTSLHSGVPS 60
DB 20 DIQWTQSPSSLSASVGDRTVITTCASQDISNYLNWYQOKPKAKPKLIYTTSLHSGVPS 79
61 RFSGSGSGDTYTLTISLSLOPEDPATYTCQOQNTLPTFGGKTVEIKRTV 110
61 RFSGSGSGDTYTLTISLSLOPEDPATYTCQOQNTLPTFGGKTVEIKRTV 129
DB 80 RFSGSGSGDTYTLTISLSLOPEDPATYTCQOQNTLPTFGGKTVEIKRTV 129

RESULT 13
US-08-437-642B-25
Sequence 25, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-25

Query Match 91.1%; Score 525; DB 3; Length 233;
Best Local Similarity 90.9%; Pred. No. 4,3e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQWTSPLSLASVGRVTTTCASQDISNYLNMWYQKRGKAPKVLITYFTSLHSGVPS 60
DB 20 DIQWTSPLSLASVGRVTTTCASQDISNYLNMWYQKRGKAPKVLITYFTSLHSGVPS 79
QY 61 RFGSGSGDTFTLTITSLQPEDFATYCCQYSTVPTFGGTKEIKRTV 110
DB 80 RFGSGSGDTFTLTITSLQPEDFATYCCQGNLTLPFTFGGTKEIKRTV 129

RESULT 14
US-08-146-206C-25
Sequence 25, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-25

Query Match 91.1%; Score 525; DB 4; Length 233;
Best Local Similarity 90.9%; Pred. No. 4,3e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQWTSPLSLASVGRVTTTCASQDISNYLNMWYQKRGKAPKVLITYFTSLHSGVPS 60
DB 20 DIQWTSPLSLASVGRVTTTCASQDISNYLNMWYQKRGKAPKVLITYFTSLHSGVPS 79
QY 61 RFGSGSGDTFTLTITSLQPEDFATYCCQYSTVPTFGGTKEIKRTV 110
DB 80 RFGSGSGDTFTLTITSLQPEDFATYCCQGNLTLPFTFGGTKEIKRTV 129

RESULT 15
US-09-705-686-25
Sequence 25, Application US/09705686
Patent No. 6639055
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-705-686-25

Query Match 91.1%; Score 525; DB 4; Length 233;
Best Local Similarity 90.9%; Pred. No. 4.3e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTYITCSASODISNINLNTYQKPKAPKVLITYFTSLHSGVPS 60
|||
Db 20 DIQMTQSPSSLSASVGDRTYITCRASODININLNTYQKPKAPKVLITYFTSLHSGVPS 79
|||
Qy 61 RPSGSGSGTDFTLTISLSLOPEDPATYTCOOYSTVPWTFGGTKVEIKRTV 110
|||
Db 80 RPSGSGSGTDYTLTISLSLOPEDPATYTCOOQNTLPPTFGGTVEIKRTV 129
|||

Search completed: March 14, 2005, 20:43:52
Job time : 23.6754 secs

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OM protein - protein search, using BW model

Run on: March 14, 2005, 20:22:02 ; Search time 41.008 Seconds
(without alignments)
884.760 Million cell updates/sec

Title: US-09-723-752b-8

Perfect score: 576
Sequence: 1 DQWTSFSSISASVGRVT.....YSTVPMFGQGTKEIKRTV 110

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgnt2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
2: /cgnt2_6/ptodata/2/pubppaa/PCR_NEW_PUB.pep.*
3: /cgnt2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
4: /cgnt2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
5: /cgnt2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
6: /cgnt2_6/ptodata/2/pubppaa/PCITS_PUBCOMB.pep.*
7: /cgnt2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
8: /cgnt2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
9: /cgnt2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
10: /cgnt2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
11: /cgnt2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
12: /cgnt2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
13: /cgnt2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
14: /cgnt2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
15: /cgnt2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
16: /cgnt2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep.*
17: /cgnt2_6/ptodata/2/pubppaa/US10D_NEW_PUB.pep.*
18: /cgnt2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
19: /cgnt2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
20: /cgnt2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	576	100.0	110	14	US-10-234-671-8
2	576	100.0	110	15	US-10-624-153-94
3	573	99.5	110	9	US-09-056-1608-107
4	573	99.5	110	9	US-09-056-1608-117
5	573	99.5	110	14	US-10-234-671-105
6	573	99.5	110	14	US-10-234-671-115
7	573	99.5	213	16	US-10-379-392-135
8	573	99.5	213	16	US-10-379-392-137
9	573	99.5	213	15	US-10-379-392-139
10	573	99.5	214	16	US-10-364-953-1
11	573	99.5	237	14	US-10-020-786-10
12	573	99.5	237	17	US-10-697-995-8
13	573	99.5	237	17	US-10-697-995-11

14	570	99.0	110	9	US-09-056-1608-105	Sequence 105, App
15	570	99.0	110	14	US-10-234-671-103	Sequence 103, App
16	569	98.8	213	16	US-10-379-392-155	Sequence 153, App
17	568	98.6	213	16	US-10-379-392-153	Sequence 153, App
18	567	98.4	108	9	US-09-056-1608-8	Sequence 8, App1
19	567	98.4	108	13	US-10-153-159-2	Sequence 2, App1
20	567	98.4	108	13	US-10-153-159-16	Sequence 16, App1
21	567	98.4	108	14	US-10-153-176-2	Sequence 2, App1
22	567	98.4	108	14	US-10-153-176-16	Sequence 16, App1
23	567	98.4	108	15	US-10-443-134A-2	Sequence 2, App1
24	567	98.4	108	15	US-10-443-134A-16	Sequence 16, App1
25	567	98.4	108	17	US-10-443-134A-127	Sequence 127, App
26	567	98.4	108	17	US-10-877-532-7	Sequence 7, App1
27	567	98.4	110	9	US-09-056-1608-103	Sequence 103, App
28	567	98.4	110	14	US-10-234-671-101	Sequence 101, App
29	567	98.4	237	9	US-09-056-1608-100	Sequence 100, App
30	567	98.4	237	14	US-10-234-671-100	Sequence 100, App
31	567	98.4	491	13	US-10-011-125-2	Sequence 2, App1
32	565	98.1	213	16	US-10-379-392-157	Sequence 157, App
33	564	97.9	108	13	US-10-153-159-4	Sequence 4, App1
34	564	97.9	108	14	US-10-153-176-4	Sequence 4, App1
35	564	97.9	108	15	US-10-443-134A-4	Sequence 4, App1
36	562	97.6	107	16	US-10-723-434-1	Sequence 1, App1
37	561	97.4	108	9	US-09-056-1608-126	Sequence 126, App
38	561	97.4	108	14	US-10-234-671-124	Sequence 124, App
39	559	97.0	107	9	US-09-056-1608-113	Sequence 13, App1
40	559	97.0	107	14	US-10-234-671-113	Sequence 13, App1
41	556	96.5	107	9	US-09-056-1608-115	Sequence 15, App1
42	556	96.5	107	14	US-10-234-671-115	Sequence 15, App1
43	556	96.5	214	15	US-10-364-953-4	Sequence 4, App1
44	555	96.4	214	15	US-10-364-953-3	Sequence 3, App1
45	554	96.2	110	9	US-09-056-1608-109	Sequence 109, App

ALIGNMENTS

RESULT 1
US-10-234-671-8
Sequence 8, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234, 671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-Apr-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-Apr-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-Aug-1997
ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-234-671-8

Query Match 100.0%; Score 576; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 8.4e-41;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWYQKPKAPKVLIVFTSSLSHSGVPS 60
DB 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWYQKPKAPKVLIVFTSSLSHSGVPS 60
QY 61 RFGSGSGTDFTLTISLQPEDPATYCCQYSTVPMFTFGGTVEIKRTV 110
DB 61 RFGSGSGTDFTLTISLQPEDPATYCCQYSTVPMFTFGGTVEIKRTV 110

RESULT 2
US-10-624-153-94
Sequence 94, Application US/10624153
Publication No. US20040086502A1
GENERAL INFORMATION:
APPLICANT: CHEN, YVONNE M.
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MULLER, YVES
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1C1
CURRENT APPLICATION NUMBER: US/10/624,153
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 09/440,781
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: US 60/108,945
PRIOR FILING DATE: 1998-11-18
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 94
LENGTH: 110
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
NAME/KEY: artificial
LOCATION: 1-110
OTHER INFORMATION: humanized antibody light chain variable domain
US-10-624-153-94

Query Match 100.0%; Score 576; DB 15; Length 110;
Best Local Similarity 100.0%; Pred. No. 8.4e-41;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWYQKPKAPKVLIVFTSSLSHSGVPS 60
DB 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWYQKPKAPKVLIVFTSSLSHSGVPS 60
QY 61 RFGSGSGTDFTLTISLQPEDPATYCCQYSTVPMFTFGGTVEIKRTV 110
DB 61 RFGSGSGTDFTLTISLQPEDPATYCCQYSTVPMFTFGGTVEIKRTV 110

RESULT 3
US-09-056-1608-107
Sequence 107, Application US/090561608
Patent No. US20020032315A1

GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,1608
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haseak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-1608-107

Query Match 99.5%; Score 573; DB 9; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.5e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWYQKPKAPKVLIVFTSSLSHSGVPS 60
DB 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWYQKPKAPKVLIVFTSSLSHSGVPS 60
QY 61 RFGSGSGTDFTLTISLQPEDPATYCCQYSTVPMFTFGGTVEIKRTV 110
DB 61 RFGSGSGTDFTLTISLQPEDPATYCCQYSTVPMFTFGGTVEIKRTV 110

RESULT 4
US-09-056-1608-117
Sequence 117, Application US/090561608
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-117

Query Match 99.5%; Score 573; DB 9; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.5e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLTNMYQQKPKGAPKVLITYFTSSLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLTNMYQQKPKGAPKVLITYFTSSLHSGVPS 60
Qy 61 RFGSGSGTDFLTITSSLPEDPATYCCQYSTVPTWTEGQTKVEIKRTV 110
Db 61 RFGSGSGTDFLTITSSLPEDPATYCCQYSTVPTWTEGQTKVEIKRTV 110

RESULT 5
US-10-234-671-105
Sequence 105, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Bacca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856

FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-10-234-671-105

Query Match 99.5%; Score 573; DB 14; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.5e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLTNMYQQKPKGAPKVLITYFTSSLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLTNMYQQKPKGAPKVLITYFTSSLHSGVPS 60
Qy 61 RFGSGSGTDFLTITSSLPEDPATYCCQYSTVPTWTEGQTKVEIKRTV 110
Db 61 RFGSGSGTDFLTITSSLPEDPATYCCQYSTVPTWTEGQTKVEIKRTV 110

RESULT 6
US-10-234-671-115
Sequence 115, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Bacca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-10-234-671-115

Query Match 99.5%; Score 573; DB 14; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.5e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGVDRVTITCSASODISNYLNMWYQKPGKAPKVLITYFTSSLSHGVPS 60
DB 1 DIQWTQSPSSLSASVGVDRVTITCSASODISNYLNMWYQKPGKAPKVLITYFTSSLSHGVPS 60
QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCQOYSTVPMWTFGGTKVEIKRTV 110
DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCQOYSTVPMWTFGGTKVEIKRTV 110

RESULT 7

US-10-379-392-135
Sequence 135, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahiyat, Basel I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 135
LENGTH: 213
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Humanized
US-10-379-392-135

Query Match 99.5%; Score 573; DB 16; Length 213;
Best Local Similarity 99.1%; Pred. No. 2.8e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGVDRVTITCSASODISNYLNMWYQKPGKAPKVLITYFTSSLSHGVPS 60
DB 1 DIQWTQSPSSLSASVGVDRVTITCSASODISNYLNMWYQKPGKAPKVLITYFTSSLSHGVPS 60
QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCQOYSTVPMWTFGGTKVEIKRTV 110
DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCQOYSTVPMWTFGGTKVEIKRTV 110

RESULT 8

US-10-379-392-137
Sequence 137, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahiyat, Basel I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843

PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 137
LENGTH: 213
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-379-392-137

Query Match

99.5%; Score 573; DB 16; Length 213;
Best Local Similarity 99.1%; Pred. No. 2.8e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGVDRVTITCSASODISNYLNMWYQKPGKAPKVLITYFTSSLSHGVPS 60
DB 1 DIQWTQSPSSLSASVGVDRVTITCSASODISNYLNMWYQKPGKAPKVLITYFTSSLSHGVPS 60
QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCQOYSTVPMWTFGGTKVEIKRTV 110
DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCQOYSTVPMWTFGGTKVEIKRTV 110

RESULT 9

US-10-379-392-139
Sequence 139, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahiyat, Basel I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 139
LENGTH: 213
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (116)..(116)
OTHER INFORMATION: Xaa at position 116 can be Phe or Tyr
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (133)..(133)
OTHER INFORMATION: Xaa at position 133 can be Ile, Met or Val
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (135)..(135)
OTHER INFORMATION: Xaa at position 135 can be Leu, Ile or Met
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (176)..(176)
OTHER INFORMATION: Xaa at position 176 can be Met, Val, Ala or Ser
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (178)..(178)
OTHER INFORMATION: Xaa at position 178 can be Met, Thr or Val
US-10-379-392-139

Query Match 99.5%; Score 573; DB 16; Length 213;
Best Local Similarity 99.1%; Pred. No. 2.8e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTGSPSSLSASVGDRTVITCSASODISNYLNMWYQKPKAKPKVLIYFTSSLHSGVPS 60
DB 1 DIQLTGSPSSLSASVGDRTVITCSASODISNYLNMWYQKPKAKPKVLIYFTSSLHSGVPS 60

QY 61 RFSGSGSGTDFTLTTLISLQPEDFATYCCQYSTVPMTFGGTKEIKRTV 110
DB 61 RFSGSGSGTDFTLTTLISLQPEDFATYCCQYSTVPMTFGGTKEIKRTV 110

RESULT 10

US-10-364-953-1
Sequence 1, Application US/10364953
Publication No. US20030224397A1
GENERAL INFORMATION:
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MARVIN, JONATHAN S.
TITLE OF INVENTION: ANTIBODY VARIANTS WITH FASTER ANTIGEN ASSOCIATION RATES
FILE REFERENCE: PI95IRI
CURRENT APPLICATION NUMBER: US/10/364,953
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/355,895
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/409,685
PRIOR FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 1
LENGTH: 214
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: Artificial Sequence
LOCATION: Full
OTHER INFORMATION: Y0101-VL
US-10-364-953-1

Query Match 99.5%; Score 573; DB 15; Length 214;
Best Local Similarity 99.1%; Pred. No. 2.8e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTGSPSSLSASVGDRTVITCSASODISNYLNMWYQKPKAKPKVLIYFTSSLHSGVPS 60
DB 1 DIQLTGSPSSLSASVGDRTVITCSASODISNYLNMWYQKPKAKPKVLIYFTSSLHSGVPS 60

QY 61 RFSGSGSGTDFTLTTLISLQPEDFATYCCQYSTVPMTFGGTKEIKRTV 110
DB 61 RFSGSGSGTDFTLTTLISLQPEDFATYCCQYSTVPMTFGGTKEIKRTV 110

RESULT 11

US-10-020-786-10
Sequence 10, Application US/10020786
Publication No. US20030073164A1
GENERAL INFORMATION:
APPLICANT: Stimmone, Laura C.
APPLICANT: Klimowski, Laura
APPLICANT: Reilly, Dorothea
APPLICANT: Yaneura, Daniel G.
TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
FILE REFERENCE: PI793RI
CURRENT APPLICATION NUMBER: US/10/020,786
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/256,164
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 10
LENGTH: 237
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:

OTHER INFORMATION: anti-VEGF light chain
US-10-020-786-10

Query Match 99.5%; Score 573; DB 14; Length 237;
Best Local Similarity 99.1%; Pred. No. 3.1e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTGSPSSLSASVGDRTVITCSASODISNYLNMWYQKPKAKPKVLIYFTSSLHSGVPS 60
DB 24 DIQLTGSPSSLSASVGDRTVITCSASODISNYLNMWYQKPKAKPKVLIYFTSSLHSGVPS 83

QY 61 RFSGSGSGTDFTLTTLISLQPEDFATYCCQYSTVPMTFGGTKEIKRTV 110
DB 84 RFSGSGSGTDFTLTTLISLQPEDFATYCCQYSTVPMTFGGTKEIKRTV 133

RESULT 12

US-10-697-995-8
Sequence 8, Application US/10697995
Publication No. US20050048572A1
GENERAL INFORMATION:
APPLICANT: Reilly, Dorothea
APPLICANT: Yaneura, Daniel G.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION
FILE REFERENCE: 11669.195USU1
CURRENT APPLICATION NUMBER: US/10/697,995
CURRENT FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: US 60/422,952
PRIOR FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 8
LENGTH: 237
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: anti-VEGF light chain
US-10-697-995-8

Query Match 99.5%; Score 573; DB 17; Length 237;
Best Local Similarity 99.1%; Pred. No. 3.1e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTGSPSSLSASVGDRTVITCSASODISNYLNMWYQKPKAKPKVLIYFTSSLHSGVPS 60
DB 24 DIQLTGSPSSLSASVGDRTVITCSASODISNYLNMWYQKPKAKPKVLIYFTSSLHSGVPS 83

QY 61 RFSGSGSGTDFTLTTLISLQPEDFATYCCQYSTVPMTFGGTKEIKRTV 110
DB 84 RFSGSGSGTDFTLTTLISLQPEDFATYCCQYSTVPMTFGGTKEIKRTV 133

RESULT 13

US-10-697-995-11
Sequence 11, Application US/10697995
Publication No. US20050048572A1
GENERAL INFORMATION:
APPLICANT: Reilly, Dorothea
APPLICANT: Yaneura, Daniel G.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION
FILE REFERENCE: 11669.195USU1
CURRENT APPLICATION NUMBER: US/10/697,995
CURRENT FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: US 60/422,952
PRIOR FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 11
LENGTH: 237
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Anti-VEGF light chain
US-10-697-995-11

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 14, 2005, 20:39:29 ; Search time 16.6447 Seconds
(without alignments)
635.867 Million cell updates/sec

Title: US-09-723-752B-8

Perfect score: 576
Sequence: 1 DIOMTOSPSLSASVGDVRT.....YSTVPMTFGGKTVEIKRTV 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	513	89.1	127	2 S40367	Ig kappa chain V-J
2	490	85.1	108	1 KIHUV	Ig kappa chain V-I
3	486	84.4	125	2 S40333	Ig kappa chain V-J
4	485	84.2	123	2 S40331	Ig kappa chain - h
5	484	84.0	108	2 S49047	Ig kappa chain V r
6	484	84.0	131	2 S44132	Ig kappa chain V-J
7	482	83.7	108	2 S44132	Ig kappa chain V r
8	482	83.7	109	2 S41998	Ig kappa chain - h
9	480	83.3	129	2 S52789	Ig kappa chain V r
10	476	82.6	129	2 S40369	Ig kappa chain - h
11	475	82.5	107	2 S36264	Ig kappa chain V
12	474	82.3	109	1 KIHUV	Ig kappa chain V-I
13	472	81.9	108	1 KIHUV	Ig kappa chain V-I
14	472	81.9	109	2 S31981	Ig kappa chain - h
15	472	81.9	111	2 A38740	Ig kappa chain V r
16	471.5	81.9	124	2 S40336	Ig kappa chain V-J
17	470	81.6	110	2 S44118	Ig kappa chain V-J
18	469	81.4	108	1 KIHUV	Ig kappa chain V-I
19	469	81.4	139	2 S40365	Ig kappa chain - h
20	468.5	81.3	107	2 S36275	Ig kappa chain V
21	468	81.2	108	2 S19674	Ig kappa chain V r
22	468	81.2	132	2 S40334	Ig kappa chain - h
23	467	81.1	108	1 KIHUV	Ig kappa chain V-I
24	467	81.1	125	2 S40339	Ig kappa chain V-J
25	466	80.9	130	2 S40368	Ig kappa chain - h
26	464	80.6	108	2 T39154	Ig kappa chain (BR
27	464	80.6	111	2 E38740	Ig kappa chain V r
28	462	80.2	108	1 KIHUV	Ig kappa chain V-I
29	462	80.2	108	1 KIHUV	Ig kappa chain V-I

30	462	80.2	111	2 C38740	Ig kappa chain V r
31	462	80.2	122	2 S40314	Ig kappa chain - h
32	462	80.2	129	2 S40317	Ig kappa chain - h
33	462	80.2	129	2 S52793	Ig kappa chain V r
34	462	80.2	135	2 S24320	Ig kappa chain pre
35	461	80.0	108	2 S47182	Ig kappa chain - h
36	460.5	79.9	125	2 S40315	Ig kappa chain - h
37	460	79.9	107	2 S36269	Ig kappa chain V
38	460	79.9	117	2 S46371	Ig kappa chain V-J
39	460	79.9	125	2 S40316	Ig kappa chain - h
40	460	79.9	129	1 KIHUV	Ig kappa chain pre
41	459	79.7	111	2 G38740	Ig kappa chain V r
42	459	79.7	117	2 S46376	Ig kappa chain V-J
43	459	79.7	122	2 S40370	Ig kappa chain - h
44	458	79.5	107	2 I69017	anti-HIV envelope
45	458	79.5	108	1 KIHUV	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

S40367
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40367
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40367
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-127 <KLE>
C/Species: Homo sapiens (man)
C/Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C/Accession: A91653; A01862; S02573
R/Schleicher, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A/Title: Die Primärstruktur einer monoklonalen Immunoglobulin-L-Kette vom kappa-Typ, Su
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 89.1%; Score 513; DB 2; Length 127;
Best Local Similarity 90.0%; Pred. No. 1.9e-38;
Matches 99; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Oy 1 DIOMTOSPSLSASVGDVRTTTCASODISNYLNTQKRGKAPKULIYFTSSLSHGSVPS 60
Db 18 DIOMTOSPSLSASVGDVRTTTCRASQISNINWYORKGKAPKULIYASSLSQSVPS 77
Oy 61 RFSGSGSGTDFLTITISLQPEDFATYCCOYSTVPMTFGGKTVEIKRTV 110
Db 78 RFSGSGSGTDFLTITISLQPEDFATYCCOYSTVPMTFGGKTVEIKRTV 127

RESULT 2

KIHUV
Ig kappa chain V-I region (Au) - human
C/Species: Homo sapiens (man)
C/Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C/Accession: A91653; A01862; S02573
R/Schleicher, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A/Title: Die Primärstruktur einer monoklonalen Immunoglobulin-L-Kette vom kappa-Typ, Su
A/Reference number: A91653; MUID:72189444; PMID:5028201
A/Accession: A91653
A/Molecule type: protein
A/Residues: 1-108 <SCH>
A/Cross-references: UNIPROT:P01594
A/Note: The C region of this chain has the Inv (3) marker
R/Phlanner, H.; Schiffer, M.; Bep, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Ste
Biophys. Struct. Mech. 1, 139-146, 1975
A/Title: The structure determination of the variable portion of the Bence-Jones protein
A/Reference number: A90729; MUID:77022433; PMID:1334024
A/Contents: annotation; X-ray crystallography

A/Note: the structure of the V region was determined by molecular replacement methods using R/Stelner, V.; Chang, J.Y.
PDB: 1ctt, 222, 6-10, 1987
A/Title: Chemical modification of the carboxyl groups of protein substrates enhances the A/Reference number: S02572; MUID:8805152; PMID:3115831
A/Content: annotation
C/Comment: This is a Bence Jones protein.
C/Genetics:
A/Gene: GDB:IGKV1
A/Cross-references: GDB:136264
A/Map position: 2p12-2p12
C/Complex: an immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds in some cases, such as Iga and Igm, the subunits associate into 16 C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>
F/23-88/Domain: heterotrimer predicted

Query Match 85.1%; Score 490; DB 1; Length 108;
Best Local Similarity 86.1%; Pred. No. 1.7e-36;
Matches 93; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVITTCASQDISNYLMWYQKPKAPKVLITFTSLHSGVPS 60
1 DIQMTSPSSLSASVGRVITTCASQDISNYLMWYQKPKAPKVLITFTSLHSGVPS 60
Db 1 DIQMTSPSSLSASVGRVITTCASQDISNYLMWYQKPKAPKVLITFTSLHSGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDPATYVCOQYSTVPMTFGGTVEIKR 108
61 RFGSGSGTDFTLTISLQPEDPATYVCOQYSTVPMTFGGTVEIKR 108
Db 61 RFGSGSGTDFTLTISLQPEDPATYVCOQYSTVPMTFGGTVEIKR 108

RESULT 3
S4033
Ig kappa chain V-J region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S4033
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
A/Title: Expressed human immunoglobulin chl genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S4033
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-125 <KLB>
A/Cross-references: EMBL:X72443; NID:G441354; PIDN:CAAS111.1; PID:G441355
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/34-108/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 486; DB 2; Length 125;
Best Local Similarity 86.0%; Pred. No. 4.5e-36;
Matches 92; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVITTCASQDISNYLMWYQKPKAPKVLITFTSLHSGVPS 60
1 DIQMTSPSSLSASVGRVITTCASQDISNYLMWYQKPKAPKVLITFTSLHSGVPS 60
Db 1 DIQMTSPSSLSASVGRVITTCASQDISNYLMWYQKPKAPKVLITFTSLHSGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDPATYVCOQYSTVPMTFGGTVEIKR 107
61 RFGSGSGTDFTLTISLQPEDPATYVCOQYSTVPMTFGGTVEIKR 107
Db 61 RFGSGSGTDFTLTISLQPEDPATYVCOQYSTVPMTFGGTVEIKR 107

RESULT 4
S40331
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40331
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
A/Title: Expressed human immunoglobulin chl genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40331
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-123 <KLB>
A/Cross-references: EMBL:X72441; NID:G441350; PIDN:CAAS1109.1; PID:G441351
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 485; DB 2; Length 123;
Best Local Similarity 88.8%; Pred. No. 5.4e-36;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVITTCASQDISNYLMWYQKPKAPKVLITFTSLHSGVPS 60
1 DIQMTSPSSLSASVGRVITTCASQDISNYLMWYQKPKAPKVLITFTSLHSGVPS 60
Db 1 DIQMTSPSSLSASVGRVITTCASQDISNYLMWYQKPKAPKVLITFTSLHSGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDPATYVCOQYSTVPMTFGGTVEIKR 107
61 RFGSGSGTDFTLTISLQPEDPATYVCOQYSTVPMTFGGTVEIKR 107
Db 61 RFGSGSGTDFTLTISLQPEDPATYVCOQYSTVPMTFGGTVEIKR 107

RESULT 5
B49047
Ig kappa chain V region (monoclonal strational autoantibody strAB SA-1A) - human (frag
C/Species: Homo sapiens (man)
C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: B49047
R/Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
A/Title: Human monoclonal strational autoantibodies isolated from thymic B lymphocytes
A/Reference number: A49047; MUID:92387224; PMID:1516616
A/Accession: B49047
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-108 <VIC>
A/Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A/Experimental source: thymic B lymphocytes
A/Note: sequence extracted from NCBI Backbone (NCBIN:113208, NCBI:113209)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 484; DB 2; Length 108;
Best Local Similarity 88.0%; Pred. No. 5.8e-36;
Matches 95; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVITTCASQDISNYLMWYQKPKAPKVLITFTSLHSGVPS 60
1 DIQMTSPSSLSASVGRVITTCASQDISNYLMWYQKPKAPKVLITFTSLHSGVPS 60
Db 1 DIQMTSPSSLSASVGRVITTCASQDISNYLMWYQKPKAPKVLITFTSLHSGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDPATYVCOQYSTVPMTFGGTVEIKR 108
61 RFGSGSGTDFTLTISLQPEDPATYVCOQYSTVPMTFGGTVEIKR 108
Db 61 RFGSGSGTDFTLTISLQPEDPATYVCOQYSTVPMTFGGTVEIKR 108

RESULT 6
S40352
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40352
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
A/Title: Expressed human immunoglobulin chl genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40352
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-131 <KLB>
A/Cross-references: EMBL:X72462; NID:G441392; PIDN:CAAS1130.1; PID:G441393
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/36-110/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 484; DB 2; Length 131;
 Best Local Similarity 85.5%; Pred. No. 7.1e-36;
 Matches 94; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNMWYQKRGKAPKVLITYFTSSLSHGVPS 60
 |||
 DB 21 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNMWYQKRGKAPKVLITYFTSSLSHGVPS 80
 |||
 QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQYSTVPMTFGGTKEIKRTV 110
 |||
 DB 81 RFSGSGSGTDFTLTISLQPEDPATYCCQKXNSVPRFGGTKEIKRTV 130
 |||

RESULT 7

844122
 Ig kappa chain V region - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_rev13-Jan-1995 #text_change 24-May-2001
 C/Accession: S44122
 R/Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
 Submitted to the EMBL Data Library, March 1994
 A/Description: Idiotype vaccination against human B-cell lymphoma: rescue of variable
 A/Reference number: S44105
 A/Accession: S44122
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-108 <HAM>
 A/Cross-references: EMBL:Z31390; NID:G472976; PIDN:CAA83265.1; PID:G940533
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C/Keywords: heterotrimer; Immunoglobulin
 F/16-90/Domain: Immunoglobulin homology <IM>

Query Match 83.7%; Score 482; DB 2; Length 108;
 Best Local Similarity 87.0%; Pred. No. 8.7e-36;
 Matches 94; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNMWYQKRGKAPKVLITYFTSSLSHGVPS 60
 |||
 DB 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNMWYQKRGKAPKVLITYFTSSLSHGVPS 60
 |||
 QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQYSTVPMTFGGTKEIKR 108
 |||
 DB 61 RFSGSGSGTDFTLTISLQPEDPATYCCQSYSTPMTFGGTKEIKR 108
 |||

RESULT 8

S31998
 Ig kappa chain - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 06-Feb-1995 #sequence_rev13-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S31998
 R/Portolano, S.; Chazenbalk, G.D.; Hutcheson, S.J.; McLachlan, S.M.; Rapoport, B.
 Submitted to the EMBL Data Library, June 1992
 A/Description: Lack of promitogenicity in autoantigen-specific H and L chain combinations as
 A/Reference number: S31977
 A/Accession: S31998
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-109 <FOR>
 A/Cross-references: EMBL:Z15081; NID:G38501; PIDN:CAA78790.1; PID:G38502
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C/Keywords: heterotrimer; Immunoglobulin
 F/16-90/Domain: Immunoglobulin homology <IM>

Query Match 83.7%; Score 482; DB 2; Length 109;
 Best Local Similarity 85.3%; Pred. No. 8.8e-36;
 Matches 93; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNMWYQKRGKAPKVLITYFTSSLSHGVPS 60
 |||
 DB 1 ELMVTQSPSSLSASVGRVTITCRASQDISAYLNMWYQKRGKAPKVLITYFTSSLSHGVPS 60
 |||

QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQYSTVPMTFGGTKEIKRT 109
 |||
 DB 61 RFSGSGSGTDFTLTISLQPEDPATYCCQSYDTPMTFGGTKEIKRT 109
 |||

RESULT 9

S52789
 Ig kappa chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1995 #sequence_rev13-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S52789
 R/Rocca, A.; Khamilich, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret,
 submitted to the EMBL Data Library, March 1995
 A/Description: Light chain V region gene usage restriction and peculiarities in myeloma-
 A/Reference number: S52789
 A/Accession: S52789
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-129 <ROC>
 A/Cross-references: EMBL:X85995; NID:G758588; PIDN:CAA5987.1; PID:G758588
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C/Keywords: heterotrimer; Immunoglobulin
 F/38-112/Domain: Immunoglobulin homology <IM>

Query Match 83.3%; Score 480; DB 2; Length 129;
 Best Local Similarity 86.0%; Pred. No. 1.6e-35;
 Matches 92; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNMWYQKRGKAPKVLITYFTSSLSHGVPS 60
 |||
 DB 23 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNMWYQKRGKAPKVLITYFTSSLSHGVPS 82
 |||
 QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQYSTVPMTFGGTKEIKR 107
 |||
 DB 83 RFSGSGSGTDFTLTISLQPEDPATYCCQYDNLPTFGGTKEIKR 129
 |||

RESULT 10

S40369
 Ig kappa chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Mar-1994 #sequence_rev13-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S40369
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin ch1 genes and their hypermutation.
 A/Reference number: S40312; WUID:94080891; PMID:8258341
 A/Accession: S40369
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-129 <KLE>
 A/Cross-references: EMBL:X72479; NID:G441426; PIDN:CAA51147.1; PID:G441427
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C/Keywords: heterotrimer; Immunoglobulin
 F/37-11/Domain: Immunoglobulin homology <IM>

Query Match 82.6%; Score 476; DB 2; Length 129;
 Best Local Similarity 85.2%; Pred. No. 3.5e-35;
 Matches 92; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNMWYQKRGKAPKVLITYFTSSLSHGVPS 60
 |||
 DB 22 DIQMTQSPSSLSASVGRVTITCRASHVTSNHLWYQKRGKAPKVLITYFTSSLSHGVPS 81
 |||

QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQYSTVPMTFGGTKEIKR 108
 |||
 DB 82 RFSGSGSGTDFTLTISLQPEDPATYCCQYNSVPTFGGTKEIKR 129
 |||

RESULT 11

S36264
 Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
 C/Species: Homo sapiens (man)

Ig kappa chain V region (Py20) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
 C/Accession: A38740
 R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
 J Biol. Chem. 266, 6607-6613, 1991
 A>Title: Heavy and light chain variable region sequences and antibody properties of anti-
 A:Reference number: A38740; WUID:91177923; PMID:1706720
 A:Accession: A38740
 A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: mRNA
 A:Residues: 1-111 <RUF>
 A:Cross-references: UNIPROT:Q91WS9
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 81.9%; Score 472; DB 2; Length 111;
 Best Local Similarity 81.5%; Pred. No. 6.8e-35;
 Matches 88; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY	1	DIQMTQSPSSLSASVGDRTVITCSAODISNYLNMWYQOKPKAKPKLITFTSLHSGVPS	60
DB	4	DVQMTQTITSSLSASLGDRTVITCSASQGISNYLNMWYQOKPKDGTVKLLIYTTSLHSGVPS	63
QY	61	RPSGSGSGTDFLTITISLQPEDFATYCCQYSTVPWTFGQTKVEIKR	108
DB	64	RPSGSGSGTDTLTISNLEPEDVATYCCQYISKVPWTFGQTKLEIKR	111

Search completed: March 14, 2005, 21:08:51
 Job time : 17.6447 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 14, 2005, 20:32:33 ; Search time 77.193 Seconds
(without alignment)

729.713 Million cell updates/sec

Title: US-09-723-752b-8
Perfect score: 576
Sequence: 1 DQWTPSSSLASASVGRVT.....YSTVPMTFGCTKYEIKRTV 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing filter 45 summaries

Database : Uniprot_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	490	85.1	108	1 KY1B_HUMAN	P01594 homo sapien
2	488	84.7	108	09UL77	O9UL77 homo sapien
3	485	84.4	236	06GKX9	O6GKX9 homo sapien
4	485	84.2	236	06GKX1	O6GKX1 homo sapien
5	484	84.0	236	07Z3Y4	O7Z3Y4 homo sapien
6	477.5	82.9	107	2 O6S8A9	O6S8A9 homo sapien
7	477	82.8	236	2 O6GKX8	O6GKX8 homo sapien
8	474	82.3	108	1 KY1H_HUMAN	P01600 homo sapien
9	474	82.3	108	1 KY1H_HUMAN	P01600 homo sapien
10	474	82.3	236	2 O6GKX0	O6GKX0 homo sapien
11	472	81.9	108	1 KY1R_HUMAN	P01607 homo sapien
12	469	81.4	108	1 KY1R_HUMAN	P01607 homo sapien
13	468	81.2	108	2 O9UL70	O9UL70 homo sapien
14	467	81.1	108	2 KY1A_HUMAN	P01593 homo sapien
15	465	80.7	234	2 O7Z473	O7Z473 homo sapien
16	463	80.4	236	2 O6PIH7	O6PIH7 homo sapien
17	462	80.2	108	1 KY1P_HUMAN	P01608 homo sapien
18	462	80.2	108	1 KY1V_HUMAN	P01608 homo sapien
19	460	79.9	129	1 KY1V_HUMAN	P01608 homo sapien
20	458	79.5	108	1 KY1E_HUMAN	P01597 homo sapien
21	457.5	79.4	107	1 KY1D_HUMAN	P01596 homo sapien
22	457	79.3	108	1 KY1M_HUMAN	P01605 homo sapien
23	456	79.2	108	1 KY1K_HUMAN	P01603 homo sapien
24	455.5	79.1	107	2 O9UL81	O9UL81 homo sapien
25	455	79.0	244	2 O6S2C8	O6S2C8 homo sapien
26	452	78.5	108	1 KY1O_HUMAN	P01609 homo sapien
27	451	78.3	108	1 KY1S_HUMAN	P01611 homo sapien
28	451	78.3	116	2 O96PF6	O96PF6 homo sapien
29	450	78.1	108	1 KY1N_HUMAN	P01606 homo sapien
30	449	78.0	108	1 KY1C_HUMAN	P01595 homo sapien
31	448	77.8	108	1 KY1J_MOUSE	P01643 mus musculu

32	448	77.8	240	2 O6S2C9	O6S2C9 homo sapien
33	446	77.4	108	1 KY1G_HUMAN	P01599 homo sapien
34	443	76.9	236	2 O6PIF5	O6PIF5 homo sapien
35	442	76.7	108	1 KY1F_HUMAN	P01598 homo sapien
36	442	76.7	108	1 KY1L_HUMAN	P01604 homo sapien
37	442	76.7	108	2 O9UL79	O9UL79 homo sapien
38	441	76.6	236	2 O6PIH4	O6PIH4 homo sapien
39	431	74.8	108	1 KY5K_MOUSE	P01644 mus musculu
40	431	74.8	108	1 KY5N_MOUSE	P01647 mus musculu
41	429	74.5	108	1 KY5L_MOUSE	P01645 mus musculu
42	429	74.5	108	1 KY5M_MOUSE	P01646 mus musculu
43	428	74.3	108	1 KY5O_MOUSE	P01648 mus musculu
44	427.5	74.2	109	1 KY1T_HUMAN	P01612 homo sapien
45	425	73.8	108	1 KY5U_MOUSE	P04946 mus musculu

ALIGNMENTS

RESULT 1
ID KY1B_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE IG kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au).";
RT Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=77022433; PubMed=1234024;
RA Fehllhammer H., Schiffer M., Bpp O., Colman P.M., Latman E.E.,
RT "The structure determination of the variable portion of the Bence-Jones protein Au.";
RT Biophys. Struct. Mech. 1:139-146(1975).
CC -1- MISCELLANEOUS: The structure of the V region was determined by molecular replacement methods using the known structure of the V region of the kappa chain RT.
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC PIR; A91653; K1HUVU.
DR PDB; 1UV5; X-ray; A=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv_1.
DR PROSITE; PSS0835; IG LIKE_1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region.
KW DOMAIN 1
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 2 34 Complementarity-determining-1.
FT DOMAIN 3 35 Framework-2.
FT DOMAIN 4 56 Complementarity-determining-2.
FT DOMAIN 5 57 Complementarity-determining-3.
FT DOMAIN 6 58 Framework-3.
FT DOMAIN 7 59 Complementarity-determining-4.
FT DOMAIN 8 60 Framework-4.
FT DISULFID 23 88 By similarity.
FT STRAND 4 5

FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 21
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108
SQ SEQUENCE 108 AA; 11939 MW; E801187BE6F6B9 CRC64;

Query Match 85.1%; Score 490; DB 1; Length 108;
Best Local Similarity 86.1%; Pred. No. 1.2e-42;
Matches 93; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIOMTQSPSSLSASVGDRTVITCSASODISNTLMNYOQKPKAPKVLITYFTSSLSHGVP 60
Db 1 DIOMTQSPSSLSASVGDRTVITCSASODISNTLMNYOQKPKAPKVLITYDASNSLSGVP 60
Qy 61 RFGSGSGCTDPTLTITSSLOPEDPATYTCQOYSTVPMFGGTKEIKR 108
Db 61 RFGSGSGAHFTFTITSSLOPEDPATYTCQOYSTVPMFGGTKEIKR 108

RESULT 2

ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjln.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berner S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; IBMW.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716CAD16F3 CRC64;

Query Match 84.7%; Score 488; DB 2; Length 108;
Best Local Similarity 87.0%; Pred. No. 2e-42;
Matches 94; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIOMTQSPSSLSASVGDRTVITCSASODISNTLMNYOQKPKAPKVLITYFTSSLSHGVP 60
Db 1 DIOMTQSPSSLSASVGDRTVITCSASODISNTLMNYOQKPKAPKVLITYFTSSLSHGVP 60

Db 1 DIOMTQSPSSLSASVGDRTVITCSASODISNTLMNYOQKPKAPKVLITYFTSSLSHGVP 60
Qy 61 RFGSGSGCTDPTLTITSSLOPEDPATYTCQOYSTVPMFGGTKEIKR 108
Db 61 RFGSGSGCTDPTLTITSSLOPEDPATYTCQOYSTVPMFGGTKEIKR 108

RESULT 3

ID Q6GMX9 PRELIMINARY; PRT; 236 AA.
AC Q6GMX9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Dichtchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshitaki S., Carrinck P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.T., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Krzywinski M.I., Skelton U., Small D.E., Scheraga A., Schein J.E.,
RA Jones S.J., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; -.
DR InterPro; IPR003599; IG_1like.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-sect; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KV Hypothetical protein.
SQ SEQUENCE 236 AA; 25924 MW; PDE2093DC560CF7 CRC64;

Query Match 84.4%; Score 486; DB 2; Length 236;
Best Local Similarity 86.4%; Pred. No. 7.8e-42;
Matches 95; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIOMTQSPSSLSASVGDRTVITCSASODISNTLMNYOQKPKAPKVLITYFTSSLSHGVP 60
Db 23 DIOMTQSPSSLSASVGDRTVITCSASODISNTLMNYOQKPKAPKVLITYFTSSLSHGVP 82
Qy 61 RFGSGSGCTDPTLTITSSLOPEDPATYTCQOYSTVPMFGGTKEIKR 110

Db 83 RFSSGSGTDFLTITSSLOPEDFATYCCOQNTYTLTGCGTKVEIKRTV 132

```
RESULT 4
ID 06GMW1 PRELIMINARY; PRT: 236 AA.
AC 06GMW1;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bock S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Straubeberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -
DR InterPro; IPR003599; IG_1
DR InterPro; IPR007110; IG_1like
DR InterPro; IPR003597; IG_1c
DR InterPro; IPR003006; IG_MHC
DR InterPro; IPR003596; IG_V
DR Pfam; PF07654; CI-bet; 1
DR Pfam; PF00047; Ig; 2
DR SMART; SM00409; IG; 2
DR SMART; SM00406; IGV; 1
DR PROSITE; PS00835; IG_LIKE; 2
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match 84.2%; Score 485; DB 2; Length 236;
Best Local Similarity 88.1%; Pred. No. 96-42; Indels 0; Gaps 0;
Matches 96; Conservative 1; Mismatches 12;
```

Db 83 RFSSGSGTDFLTITSSLOPEDFATYCCOQNTYTLTGCGTKVEIKRTV 132

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RESULT 5
ID 0723Y4 PRELIMINARY; PRT: 236 AA.
AC 0723Y4;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bock S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Straubeberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -
DR HSSP; P01834; 1HEZ
DR InterPro; IPR007110; IG_1like
DR InterPro; IPR003597; IG_1c
DR InterPro; IPR003006; IG_MHC
DR InterPro; IPR003596; IG_V
DR Pfam; PF07654; CI-bet; 1
DR SMART; SM00406; IGV; 1
DR PROSITE; PS00835; IG_LIKE; 2
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match 84.0%; Score 484; DB 2; Length 236;
Best Local Similarity 86.4%; Pred. No. 1,36-41; Indels 0; Gaps 0;
Matches 95; Conservative 4; Mismatches 11;
```

DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, last annotation update)
 DE Anti-streptococcal/anti-mycosin immunoglobulin kappa light chain
 DE variable region (Fragment)
 OS Homo sapiens (Human)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
 RT "Molecular analysis of polyclonal monoclonal antibodies from
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mycosin
 RT antibody V region genes."
 RL J. Immunol. 161:2020-2031(1998).
 DR EMBL: U96396; AAB6785.1; -
 DR PIR: B49047; B49047.
 DR PIR: PH0867; PH0867.
 DR PIR: S16840; S16840.
 DR PIR: S31977; S31977.
 DR PIR: S34083; S34083.
 DR PIR: S34086; S34086.
 DR HSSP: P01607; 1BMW.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003596; IG_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT TER 1
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;

Query Match 82.9%; Score 477.5; DB 2; Length 107;
 Best Local Similarity 89.0%; Pred. No. 2,3e-41;
 Matches 97; Conservative 3; Mismatches 6; Indels 3; Gaps 2;

Qy 1 DIQQTGSSSSASVGVDRVITTCASODISNYLWYQKPKAPKVLTYFTSSLSHGVS 60
 Db 1 DIQQTGSSSSASVGVDRVITTCASODISNYLWYQKPKAPKVLTYFTSSLSHGVS 60
 61 RFSSGSGTDPFTLTSSLOPEDFATYYCCQ-QYSTVPMFTFGOSTKYEIKR 108
 61 RFSSGSGTDPFTLTSSLOPEDFATYYCCQ-QYSTVPMFTFGOSTKYEIKR 107

RESULT 7
 O6GMX8 PRELIMINARY; PRT; 236 AA.
 AC O6GMX8.
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Pelting E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Kane S.S., Loguercio N.A., Pecere G.J., Abramson R.D., Mullins S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Mazy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kravynski M.I., Skaleck J., Smalick D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC073764; AAH73764.1; -
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF07654; C1-ect; 1.
 DR Pfam: PF00047; IG; 2.
 DR SMART: SM00409; IGV; 2.
 DR SMART: SM00407; IGV; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 2.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25707 MW; 4FCB814B6559EFC9 CRC64;

Query Match 82.8%; Score 477; DB 2; Length 236;
 Best Local Similarity 84.5%; Pred. No. 6,6e-41;
 Matches 93; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQQTGSSSSASVGVDRVITTCASODISNYLWYQKPKAPKVLTYFTSSLSHGVS 60
 Db 23 DIQQTGSSSSASVGVDRVITTCASODISNYLWYQKPKAPKVLTYFTSSLSHGVS 82
 61 RFSSGSGTDPFTLTSSLOPEDFATYYCCQ-QYSTVPMFTFGOSTKYEIKRTV 110
 83 RFSSGSGTDPFTLTSSLOPEDFATYYCCQ-QHSPFTFGPKVDIKRTV 132

RESULT 8
 K1H1_HUMAN STANDARD; PRT; 108 AA.
 ID K1H1_HUMAN
 AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, last sequence update)
 DT 25-OCT-2004 (Rel. 45, last annotation update)
 DS Ig kappa chain V-I region Hau.
 OS Homo sapiens (Human)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=71032830; PubMed=4097974;
 RA Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
 RT subgroups."
 RL Hoppe-Seyler G.Z. Physiol. Chem. 351:1291-1295(1970).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR: A01868; K1HUVU.
 DR PDB: 1P6L; X-ray; L=1-108.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IGV; 1.
 DR SMART: SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.
 KM 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A61608D0618 CRC64;
 Query Match 82.3%; Score 474; DB 1; Length 108;
 Best Local Similarity 86.1%; Pred. No. 5,4e-41;
 Matches 93; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 QY 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWYQKRGKAPKVLITYFTSSLSHGVS 60
 DB 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWYQKRGKAPKVLITYFTSSLSHGVS 60
 QY 61 RFSGSSSGTDFTLTISLQPEDPATYCCQYSTVPMTFGGGTVEIKR 108
 DB 61 RFSGSSSGTDFTLTISLQPEDPATYCCQYSTVPMTFGGGTVEIKR 108
 RESULT 9
 KLVY HUMAN STANDARD; PRT; 108 AA.
 ID P80362;
 AC 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 1g kappa chain V-I region WAT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RA MEDLINE-95086080; PubMed=7939311;
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
 RA Solomon A., Stevens F.J., Schiffer M.,
 RT "Comparison of crystal structures of two homologous proteins:
 RT structural origin of altered domain interactions in Immunoglobulin
 RT light-chain dimers.";
 RL Biochemistry 33:14848-14857(1994).
 RN [2]
 RP SEQUENCE OF 1-35.
 RA MEDLINE-61267384; PubMed=6167731;
 RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
 RA Popp R.A., Solomon A.,
 RT "Characterization and preliminary crystallographic data on the VL-
 RT related fragment of the human kappa Bence Jones protein Wat.";
 RL J. Mol. Biol. 147:185-193(1991).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PDB; 1KTL; X-ray; A/Bel-108.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR003110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; Icy_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.

FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT CONFLICT 30 31 TN -> SD (in Ref. 2).
 FT STRAND 4 7
 FT STRAND 10 13
 FT TURN 15 16
 FT STRAND 19 25
 FT TURN 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 45 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 84 90
 FT STRAND 98 98
 FT STRAND 102 106
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;
 Query Match 82.3%; Score 474; DB 1; Length 108;
 Best Local Similarity 83.3%; Pred. No. 5,4e-41;
 Matches 90; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
 QY 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWYQKRGKAPKVLITYFTSSLSHGVS 60
 DB 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWYQKRGKAPKVLITYFTSSLSHGVS 60
 QY 61 RFSGSSSGTDFTLTISLQPEDPATYCCQYSTVPMTFGGGTVEIKR 108
 DB 61 RFSGSSSGTDFTLTISLQPEDPATYCCQYSTVPMTFGGGTVEIKR 108
 RESULT 10
 ID Q6GMXO
 AC Q6GMXO; PRELIMINARY; PRT; 236 AA.
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Umed T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lotteliello N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbe R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schenck A., Schenck J.E.,
 RA Jones S.J., Meira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RC SEQUENCE FROM N.A.
 RA TISSUE=Spleen;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC073775; AAH73775.1; -.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-1like.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF07654; C1-sect; 1.
 DR Pfam: PF00447; IG; 2.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IGc1; 1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PSS0835; IG LIKE; 2.
 DR PROSITE: PSS0230; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25807 MW; 864BA08C7E92BFA8 CRC64;
 Query Match 82.3%; Score 474; DB 2; Length 236;
 Best Local Similarity 83.6%; Pred. No. 1,3e-40; Mismatches 12; Indels 0; Gaps 0;
 Matches 92; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNMYQOKPKAPKVLITYFTSSLSHGVS 60
 DB 23 DIQMTQSPSSLSASVGRVTITCRASQINNNYLNMYQKPKAPKVLITYFTSSLSHGVS 82
 QY 61 RFGSGSGDTFTLTISLQPEDPATYCCQYSTVPMTEGQGTKEIKRTV 110
 DB 83 RFGSGSGDTFTLTISLQPEDPATYCCQYSTVPMTEGQGTKEIKRTV 132
 RESULT 11
 KVI0_HUMAN STANDARD; PRT; 108 AA.
 ID KVI0_HUMAN
 AC P01610;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update).
 DE Ig kappa chain V-I region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=63273707; PubMed=6410398;
 RA Goni F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM
 (protein WEA) with antibody activity against 3,4-pyruvylated galactose
 in Klebsiella polysaccharides K30 and K33";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC -1- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
 against 3,4-pyruvylated galactose and isolated from a patient with
 CC Waldenstrom's macroglobulinemia.
 DR PIR: A01876; KIHUME.
 DR HSSP: P80362; 1MTL.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-1like.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00447; IG; 1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PSS0835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region;
 KM Monoclonal antibody.
 FT DOMAIN 1 23 Framework-1.
 FT 24 34 Complementarity-determining-1.

FT DOMAIN 35 49 Framework-2.
 FT 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT 89 97 Framework-3.
 FT DOMAIN 98 107 Complementarity-determining-3.
 FT DISULFID 23 88 Framework-4.
 FT NON TER 108 By similarity.
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;
 Query Match 81.9%; Score 472; DB 1; Length 108;
 Best Local Similarity 84.3%; Pred. No. 8.7e-41; Mismatches 12; Indels 0; Gaps 0;
 Matches 91; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNMYQOKPKAPKVLITYFTSSLSHGVS 60
 DB 1 DIQMTQSPSSLSASVGRVTITCRASQGRNDLTWYQOKPKAPKVLITYFTSSLSHGVS 60
 QY 61 RFGSGSGDTFTLTISLQPEDPATYCCQYSTVPMTEGQGTKEIKR 108
 DB 61 RFGSGSGDTFTLTISLQPEDPATYCCQYSTVPMTEGQGTKEIKR 108
 RESULT 12
 KVI0_HUMAN STANDARD; PRT; 108 AA.
 ID KVI0_HUMAN
 AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig kappa chain V-I region Rel.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76023758; PubMed=809329;
 RA Palm W., Hilschmann N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin
 kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
 RT and characterization of the tryptic peptides; the complete amino acid
 RT sequence of the protein; a contribution to the elucidation of the
 RT three-dimensional structure of antibodies, in particular their
 RT combining site";
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=76039968; PubMed=1182131;
 RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
 RT "The molecular structure of a dimer composed of the variable portions
 RT of the Bence-Jones protein Rel refined at 2.0-A resolution";
 RL Biochemistry 14:4943-4952(1975).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 CC marker.
 DR PIR: A91663; KIHURS.
 DR PDB: 1AR2; X-ray; @=1-107.
 DR PDB: 1BW1; X-ray; A/B=1-107.
 DR PDB: 1REI; X-ray; A/B=1-107.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-1like.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00447; IG; 1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PSS0835; IG LIKE; 1.
 KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT 24 34 Complementarity-determining-1.
 FT 35 49 Framework-2.
 FT 50 56 Complementarity-determining-2.

FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DISULFID 98 107 Framework-4.
 FT STRAND 23 88
 FT STRAND 4 7
 FT STRAND 10 13
 FT TURN 15 16
 FT STRAND 19 25
 FT TURN 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 45 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 84 90
 FT STRAND 97 98
 FT STRAND 102 106
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 81.4%; Score 469; DB 1; Length 108;
 Best Local Similarity 81.5%; Pred. No. 1.8e-40;
 Matches 88; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITTCASQDISNLYNMYOQKPKAKVLYFTSSLHSGVPS 60
 DB 1 DIQMTSPSSLSASVGDRTVITTCASQDISNLYNMYOQKPKAKVLYFTSSLHSGVPS 60
 QY 61 RFGSGSGTDFLTITSSLOPEDPATYTCQOYSTVPMPTFGGKTVEIKR 108
 DB 61 RFGSGSGTDFLTITSSLOPEDPATYTCQOYSTVPMPTFGGKTVEIKR 108

RESULT 13

QY 09UL70 PRELIMINARY; PRT; 108 AA.
 AC 09UL70;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M., Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL, AF035044; AAD56280.1; -.
 DR PIR, PH0863; PH0863.
 DR HSSP, P01607; 1BMW.
 DR InterPro: IPR007110; IG-like.
 DR SMART, SM00406; IGV, 1.
 DR SMART, SM00406; IGV, 1.
 DR PROSITE, PS50835; IG-LIKE; 1.
 FT NON_TER 1 1
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 Best Local Similarity 84.3%; Pred. No. 2.2e-40;

Matches 91; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
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 DB 1 DIQMTSPSSLSASVGDRTVITTCASQDISNLYNMYOQKPKAKVLYFTSSLHSGVPS 60
 QY 61 RFGSGSGTDFLTITSSLOPEDPATYTCQOYSTVPMPTFGGKTVEIKR 108
 DB 61 RFGSGSGTDFLTITSSLOPEDPATYTCQOYSTVPMPTFGGKTVEIKR 108

RESULT 14

KVLA_HUMAN STANDARD; PRT; 108 AA.
 ID KVLA_HUMAN
 AC P01573;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region AG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=69234734; PubMed=4893682;
 RA Tiltan K., Shinoda T., Putnam F.W.;
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges".
 RL J. Biol. Chem. 244:3550-3560(1969).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 DR PIR, A01861; K1HNG.
 DR HSSP, P01607; 1BMW.
 DR GO, GO:0005576; C:extracellular; NAS.
 DR GO, GO:0003823; F:antigen binding; NAS.
 DR GO, GO:0006955; P:immune response; NAS.
 DR InterPro: IPR003586; IG-like.
 DR SMART, SM00406; IGV, 1.
 DR PIR, P00047; 1G, 1.
 DR SMART, SM00406; IGV, 1.
 DR PROSITE, PS50835; IG-LIKE; 1.
 KW Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DISULFID 98 107 Framework-4.
 FT NON_TER 108 108
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Query Match 81.1%; Score 467; DB 1; Length 108;
 Best Local Similarity 82.4%; Pred. No. 2.8e-40;
 Matches 89; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

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 DB 1 DIQMTSPSSLSASVGDRTVITTCASQDISNLYNMYOQKPKAKVLYFTSSLHSGVPS 60
 QY 61 RFGSGSGTDFLTITSSLOPEDPATYTCQOYSTVPMPTFGGKTVEIKR 108
 DB 61 RFGSGSGTDFLTITSSLOPEDPATYTCQOYSTVPMPTFGGKTVEIKR 108

RESULT 15

QY 07Z473 PRELIMINARY; PRT; 234 AA.
 ID 07Z473;
 AC 07Z473;
 DT 01-OCT-2003 (TREMblrel. 25, Created)

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DT 01-OCT-2003 (TrEMBLrel. 25, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadiri T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=lung;
RA Strausberg R.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
DR HSP; P01834; IHEZ.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-bez; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

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Search completed: March 14, 2005, 20:49:18
 Job time : 77.193 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model1

Run on: March 14, 2005, 20:22:02 ; Search time 43.9912 Seconds
(without alignments)
884.760 Million cell updates/sec

Title: US-09-723-752B-7

Perfect score: 655
Sequence: 1 EVGLVSGGGLVPGGSLRL.....YPHYSSSHYFDWGGCTL 118

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 1396920 seqs, 32984858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

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18: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	655	100.0	118 9 US-09-056-160B-108	Sequence 108, App
2	655	100.0	118 14 US-10-234-671-7	Sequence 7, Appl
3	655	100.0	118 14 US-10-234-671-106	Sequence 106, App
4	655	100.0	118 15 US-10-624-153-96	Sequence 96, Appl
5	655	100.0	123 9 US-09-056-160B-7	Sequence 7, Appl
6	655	100.0	123 13 US-10-153-159-1	Sequence 1, Appl
7	655	100.0	123 13 US-10-153-159-14	Sequence 14, Appl
8	655	100.0	123 14 US-10-153-176-1	Sequence 14, Appl
9	655	100.0	123 14 US-10-153-176-14	Sequence 14, Appl
10	655	100.0	123 15 US-10-443-134A-1	Sequence 14, Appl
11	655	100.0	123 15 US-10-443-134A-14	Sequence 14, Appl
12	655	100.0	123 16 US-10-723-434-55	Sequence 55, Appl
13	655	100.0	123 17 US-10-877-532-8	Sequence 8, Appl

14	655	100.0	231 15 US-10-364-953-2	Sequence 2, Appl
15	651	99.4	118 9 US-09-056-160B-110	Sequence 110, App
16	651	99.4	118 14 US-10-234-671-108	Sequence 108, App
17	650	99.2	123 15 US-10-443-134A-126	Sequence 126, App
18	650	99.2	123 16 US-10-723-434-104	Sequence 129, App
19	649	99.1	123 16 US-10-443-134A-129	Sequence 129, App
20	649	99.1	123 16 US-10-723-434-70	Sequence 103, App
21	646	98.6	123 16 US-10-723-434-103	Sequence 59, App
22	645	98.5	123 16 US-10-723-434-59	Sequence 112, App
23	644	98.3	118 9 US-09-056-160B-112	Sequence 110, App
24	644	98.3	118 14 US-10-234-671-110	Sequence 97, App
25	644	98.3	118 15 US-10-624-153-97	Sequence 128, App
26	644	98.3	123 15 US-10-443-134A-128	Sequence 105, App
27	644	98.3	123 16 US-10-723-434-105	Sequence 16, Appl
28	644	98.3	231 15 US-10-364-953-5	Sequence 69, Appl
29	643	98.2	123 16 US-10-723-434-69	Sequence 114, App
30	642	98.0	118 9 US-09-056-160B-114	Sequence 112, App
31	642	98.0	118 14 US-10-234-671-112	Sequence 65, Appl
32	642	98.0	123 16 US-10-723-434-65	Sequence 16, Appl
33	638	97.4	123 9 US-09-056-160B-16	Sequence 16, Appl
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35	638	97.4	123 15 US-10-443-134A-130	Sequence 67, App
36	638	97.4	123 16 US-10-723-434-67	Sequence 101, App
37	638	97.4	123 16 US-10-723-434-101	Sequence 102, App
38	638	97.4	123 16 US-10-723-434-102	Sequence 9, Appl
39	638	97.4	231 15 US-10-364-953-9	Sequence 104, App
40	637	97.3	118 9 US-09-056-160B-106	Sequence 131, App
41	637	97.3	118 14 US-10-234-671-104	Sequence 75, Appl
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ALIGNMENTS

RESULT 1
US-09-056-160B-108
; Sequence 108, Application US/09056160B
; Patent No. US2002003215A1
; GENERAL INFORMATION:
; APPLICANT: Beca, Manuel
; APPLICANT: Wells, Manuel A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-Aug-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Haack, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1039R2
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-1608-108

Query Match 100.0%; Score 655; DB 9; Length 118;
Best Local Similarity 100.0%; Pred. No. 2,1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 EVOLVESGGGLVOPGSLRLSCAASGYFTFTYGNMWRQAPGKLEWYGMINTYTGEPY 60
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DB 61 AADFKRRFTFSLDTSKSTAYLQNMNSLRADTAIVYCAKPHYGSSHWYFDWGGTL 118

RESULT 2

US-10-234-671-7
Sequence 7, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:

APPLICANT: Baca, Manuel

Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpacin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671

FILING DATE: 03-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160

FILING DATE: 06-APR-1998

APPLICATION NUMBER: 60/126446

FILING DATE: 07-APR-1997

APPLICATION NUMBER: 60/054856

FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093R2C1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-234-671-7

Query Match 100.0%; Score 655; DB 14; Length 118;

Best Local Similarity 100.0%; Pred. No. 2,1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 EVOLVESGGGLVOPGSLRLSCAASGYFTFTYGNMWRQAPGKLEWYGMINTYTGEPY 60
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RESULT 3

US-10-234-671-106
Sequence 106, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:

APPLICANT: Baca, Manuel

Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpacin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671

FILING DATE: 03-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160

FILING DATE: 06-APR-1998

APPLICATION NUMBER: 60/126446

FILING DATE: 07-APR-1997

APPLICATION NUMBER: 60/054856

FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093R2C1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 106:

US-10-234-671-106

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Best Local Similarity 100.0%; Pred. No. 2,1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 EVOLVESGGGLVOPGSLRLSCAASGYFTFTYGNMWRQAPGKLEWYGMINTYTGEPY 60
QY 61 AADFKRRFTFSLDTSKSTAYLQNMNSLRADTAIVYCAKPHYGSSHWYFDWGGTL 118
DB 61 AADFKRRFTFSLDTSKSTAYLQNMNSLRADTAIVYCAKPHYGSSHWYFDWGGTL 118

RESULT 4
US-10-624-153-96
Sequence 96, Application US/10624153
Publication No. US20040086502A1
GENERAL INFORMATION:
APPLICANT: CHEN, YVONNE M.
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MULLER, YVES
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1C
CURRENT APPLICATION NUMBER: US/10/624,153
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 09/440,761
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: US 60/108,945
PRIOR FILING DATE: 1998-11-18
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 96
LENGTH: 118
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
NAME/KEY: artificial
LOCATION: 1-118
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-10-624-153-96

Query Match 100.0%; Score 655; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 AADFKRRFTPSLDTSKSTAYLQWNSLRADTAIVYCAKPHYGGSSHWYFDVWGQGL 118

RESULT 5
US-09-056-160B-7
Sequence 7, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, Manuel A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9861
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-7

Query Match 100.0%; Score 655; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 AADFKRRFTPSLDTSKSTAYLQWNSLRADTAIVYCAKPHYGGSSHWYFDVWGQGL 118

RESULT 6
US-10-153-159-1
Sequence 1, Application US/10153159
Publication No. US20020177170A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
APPLICANT: Heisen, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Calli
TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIE
FILE REFERENCE: 26050-704
CURRENT APPLICATION NUMBER: US/10/153,159
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of parental anti-VEGF antibody
US-10-153-159-1

Query Match 100.0%; Score 655; DB 13; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVESGGGLVQPGGSLRLSCAASGTTFTNGMMWVRQAPGKGLVWGIMINTYTSPT 60
1 EVOLVESGGGLVQPGGSLRLSCAASGTTFTNGMMWVRQAPGKGLVWGIMINTYTSPT 60
DB 61 AADFKRRFTPSLDTSKSTAYLQWNSLRADTAIVYCAKPHYGGSSHWYFDVWGQGL 118
61 AADFKRRFTPSLDTSKSTAYLQWNSLRADTAIVYCAKPHYGGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTPSLDTSKSTAYLQWNSLRADTAIVYCAKPHYGGSSHWYFDVWGQGL 118

RESULT 7
US-10-153-159-14
Sequence 14, Application US/10153159

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Publication No. US20020177170A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
APPLICANT: Heien, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Calli
TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIB
FILE REFERENCE: 26050-704
CURRENT APPLICATION NUMBER: US/10/153,159
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of AM2-ccfv
US-10-153-159-14

Query Match      100.0%; Score 655; DB 13; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYSYFTNYGMNWRQAPGKGLVWGMINITYGSEPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYSYFTNYGMNWRQAPGKGLVWGMINITYGSEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGGSSHWYFDVWGQGL 118

RESULT 8
US-10-153-176-1
Sequence 1, Application US/10153176
Publication No. US20030022240A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
APPLICANT: Heien, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Calli
APPLICANT: Cao, Yicheng
APPLICANT: Li, Shengfeng
APPLICANT: Liu, Shengjiang
TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
FILE REFERENCE: 26050-701
CURRENT APPLICATION NUMBER: US/10/153,176
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of parental anti-VEGF antibody
US-10-153-176-1

Query Match      100.0%; Score 655; DB 14; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYSYFTNYGMNWRQAPGKGLVWGMINITYGSEPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYSYFTNYGMNWRQAPGKGLVWGMINITYGSEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGGSSHWYFDVWGQGL 118
```

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Publication No. US20030022240A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
APPLICANT: Heien, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Calli
APPLICANT: Cao, Yicheng
APPLICANT: Li, Shengfeng
APPLICANT: Liu, Shengjiang
TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
FILE REFERENCE: 26050-709
CURRENT APPLICATION NUMBER: US/10/443,134A
CURRENT FILING DATE: 2003-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 126
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of AM2-ccfv
US-10-153-176-14

Query Match      100.0%; Score 655; DB 14; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYSYFTNYGMNWRQAPGKGLVWGMINITYGSEPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYSYFTNYGMNWRQAPGKGLVWGMINITYGSEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGGSSHWYFDVWGQGL 118

RESULT 9
US-10-153-176-14
Sequence 14, Application US/10153176
Publication No. US20030022240A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
APPLICANT: Heien, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Calli
APPLICANT: Cao, Yicheng
APPLICANT: Li, Shengfeng
APPLICANT: Liu, Shengjiang
TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
FILE REFERENCE: 26050-701
CURRENT APPLICATION NUMBER: US/10/153,176
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of AM2-ccfv
US-10-153-176-14

Query Match      100.0%; Score 655; DB 14; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYSYFTNYGMNWRQAPGKGLVWGMINITYGSEPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYSYFTNYGMNWRQAPGKGLVWGMINITYGSEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGGSSHWYFDVWGQGL 118

RESULT 10
US-10-443-134A-1
Sequence 134A, Application US/10443134A
Publication No. US20040010376A1
GENERAL INFORMATION:
APPLICANT: Luo, Feizhi
APPLICANT: Heien, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Calli
APPLICANT: Cao, Yicheng
APPLICANT: Li, Shengfeng
APPLICANT: Liu, Shengjiang
TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
FILE REFERENCE: 26050-709
CURRENT APPLICATION NUMBER: US/10/443,134A
CURRENT FILING DATE: 2003-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 126
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of AM2-ccfv
US-10-153-176-159
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PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of parental anti-VEGF antibody
US-10-443-134A-1

Query Match 100.0%; Score 655; DB 15; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGTTFTYGMNWVROAPGKLEWVGWINTYTGEPT 60
DB 1 EVOLVESGGGLVOPGSLRLSCAASGTTFTYGMNWVROAPGKLEWVGWINTYTGEPT 60
QY 61 AADPKRFTFSLDTSKSTAYLQWNSLRADTAIVYCAKYPHYGSSHWYFDVWGQGL 118
DB 61 AADPKRFTFSLDTSKSTAYLQWNSLRADTAIVYCAKYPHYGSSHWYFDVWGQGL 118

RESULT 11
US-10-443-134A-14
Sequence 14, Application US/10443134A
Publication No. US20040010376A1
GENERAL INFORMATION:
APPLICANT: Luo, Peizhi
APPLICANT: Heieh, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Caoli
APPLICANT: Cao, Yicheng
APPLICANT: Liu, Shengjiang
TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
FILE REFERENCE: 26050-709
CURRENT APPLICATION NUMBER: US/10/443,134A
CURRENT FILING DATE: 2003-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 10/153,176
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/153,159
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of AM2-ccFv
US-10-443-134A-14

Query Match 100.0%; Score 655; DB 15; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGTTFTYGMNWVROAPGKLEWVGWINTYTGEPT 60
DB 1 EVOLVESGGGLVOPGSLRLSCAASGTTFTYGMNWVROAPGKLEWVGWINTYTGEPT 60
QY 61 AADPKRFTFSLDTSKSTAYLQWNSLRADTAIVYCAKYPHYGSSHWYFDVWGQGL 118
DB 61 AADPKRFTFSLDTSKSTAYLQWNSLRADTAIVYCAKYPHYGSSHWYFDVWGQGL 118

RESULT 12
US-10-723-434-55
Sequence 55, Application US/10723434

Publication No. US20040133357A1
GENERAL INFORMATION:
APPLICANT: Zhong, Pingyu
APPLICANT: Luo, Peizhi
APPLICANT: Wang, Kevin C.
APPLICANT: Heieh, Mark
APPLICANT: Li, Yan
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
FILE REFERENCE: 26050-709 501
CURRENT APPLICATION NUMBER: US/10/723,434
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 10/153,176
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/443,134
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn version 3.1
SEQ ID NO 55
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH
US-10-723-434-55

Query Match 100.0%; Score 655; DB 16; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGTTFTYGMNWVROAPGKLEWVGWINTYTGEPT 60
DB 1 EVOLVESGGGLVOPGSLRLSCAASGTTFTYGMNWVROAPGKLEWVGWINTYTGEPT 60
QY 61 AADPKRFTFSLDTSKSTAYLQWNSLRADTAIVYCAKYPHYGSSHWYFDVWGQGL 118
DB 61 AADPKRFTFSLDTSKSTAYLQWNSLRADTAIVYCAKYPHYGSSHWYFDVWGQGL 118

RESULT 13
US-10-877-532-8
Sequence 8, Application US/10877532
Publication No. US20050038231A1
GENERAL INFORMATION:
APPLICANT: FAHRNER, ROBERT L.
APPLICANT: LAVERDIERE, AMY
APPLICANT: MCDONALD, PAUL J.
APPLICANT: O'LEARY, RHONA M.
TITLE OF INVENTION: REDUCING PROTEIN A LEACHING DURING PROTEIN A AFFINITY CHROMATOGR
FILE REFERENCE: P2015R1
CURRENT APPLICATION NUMBER: US/10/877,532
CURRENT FILING DATE: 2004-06-24
PRIOR APPLICATION NUMBER: US 60/490,500
PRIOR FILING DATE: 2003-07-28
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 8
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-10-877-532-8

Query Match 100.0%; Score 655; DB 17; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGTTFTYGMNWVROAPGKLEWVGWINTYTGEPT 60
DB 1 EVOLVESGGGLVOPGSLRLSCAASGTTFTYGMNWVROAPGKLEWVGWINTYTGEPT 60

QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRABDTAVYYCAKPHYGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRABDTAVYYCAKPHYGSSHWYFDVWGQGL 118

RESULT 14

US-10-364-953-2
Sequence 2, Application US/10364953
Publication No. US20030224397A1
GENERAL INFORMATION:
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MARVIN, JONATHAN S.
TITLE OF INVENTION: ANTIBODY VARIANTS WITH FASTER ANTIGEN ASSOCIATION RATES
FILE REFERENCE: P1951R1
CURRENT APPLICATION NUMBER: US/10/364,953
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/355,895
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/409,685
PRIOR FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 2
LENGTH: 231
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: Artificial Sequence
LOCATION: Full
OTHER INFORMATION: Y0101-VH
US-10-364-953-2

Query Match 100.0%; Score 655; DB 15; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.8e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVSGGGLVQPGSLRLSCAASGYFTFTNGMNVROAPGKLEWVGWINTYTGEPTY 60
DB 1 EVOLVSGGGLVQPGSLRLSCAASGYFTFTNGMNVROAPGKLEWVGWINTYTGEPTY 60
QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRABDTAVYYCAKPHYGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRABDTAVYYCAKPHYGSSHWYFDVWGQGL 118

RESULT 15

US-09-056-160B-110
Sequence 110, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-110

Query Match 99.4%; Score 651; DB 9; Length 118;
Best Local Similarity 99.2%; Pred. No. 4.4e-47;
Matches 117; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVSGGGLVQPGSLRLSCAASGYFTFTNGMNVROAPGKLEWVGWINTYTGEPTY 60
DB 1 EVOLVSGGGLVQPGSLRLSCAASGYFTFTNGMNVROAPGKLEWVGWINTYTGEPTY 60
QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRABDTAVYYCAKPHYGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRABDTAVYYCAKPHYGSSHWYFDVWGQGL 118

Search completed: March 14, 2005, 20:42:11
Job time: 44.9912 sec

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OW protein - protein search, using sw model

Run on: March 14, 2005, 20:30:13, Search time 24.3246 Seconds
(without alignments)
362.127 Million cell updates/sec

Title: US-09-723-752b-7

Perfect score: 655

Sequence: 1 EVOLVESGGGLVOPGSLRL.....YPHYSSHHWYFDVWGQCTL 118

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: Issued Patents AA: *
2: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/6CTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	100.0	118	4	US-09-440-781-96
2	644	98.3	118	4	US-09-440-781-97
3	631.5	96.4	121	4	US-09-440-781-98
4	631	96.3	491	4	US-10-011-125A-2
5	620.5	94.7	121	4	US-09-440-781-99
6	513.5	78.4	118	1	US-08-425-336-126
7	513.5	78.4	118	1	US-08-488-113B-126
8	513.5	78.4	118	1	US-08-477-484B-126
9	513.5	78.4	118	2	US-08-646-360-126
10	513.5	78.4	118	3	US-08-839-765-126
11	513.5	78.4	118	3	US-09-136-389-126
12	513.5	78.4	118	3	US-09-610-838-126
13	513.5	78.4	118	4	US-09-711-485-126
14	513.5	78.4	240	1	US-08-488-113B-147
15	513.5	78.4	240	1	US-08-488-113B-148
16	513.5	78.4	240	1	US-08-477-484B-147
17	513.5	78.4	240	1	US-08-477-484B-148
18	513.5	78.4	240	2	US-08-646-360-147
19	513.5	78.4	240	2	US-08-646-360-148
20	513.5	78.4	240	3	US-08-839-765-147
21	513.5	78.4	240	3	US-08-839-765-148
22	513.5	78.4	240	3	US-09-136-389-147
23	513.5	78.4	240	3	US-09-136-389-148
24	513.5	78.4	240	3	US-09-610-838-147
25	513.5	78.4	240	3	US-09-610-838-148
26	513.5	78.4	240	4	US-09-711-485-147
27	513.5	78.4	240	4	US-09-711-485-148

28	499.5	76.3	118	1	US-08-107-669D-29	Sequence 29, Appl
29	499.5	76.3	118	1	US-08-472-788A-29	Sequence 29, Appl
30	499.5	76.3	118	2	US-08-477-531B-29	Sequence 29, Appl
31	499.5	76.3	118	2	US-08-082-842A-29	Sequence 29, Appl
32	498.5	76.1	118	1	US-08-107-669D-67	Sequence 67, Appl
33	498.5	76.1	118	1	US-08-472-788A-89	Sequence 89, Appl
34	498.5	76.1	118	2	US-08-477-531B-67	Sequence 67, Appl
35	498.5	76.1	118	2	US-08-082-842A-89	Sequence 89, Appl
36	496.5	75.8	122	2	US-07-934-373C-20	Sequence 20, Appl
37	496.5	75.8	122	3	US-08-437-642B-20	Sequence 20, Appl
38	496.5	75.8	122	4	US-08-146-206C-20	Sequence 20, Appl
39	496.5	75.8	122	4	US-09-705-686-20	Sequence 20, Appl
40	496.5	75.8	122	4	US-09-705-392A-20	Sequence 20, Appl
41	496.5	75.8	122	4	US-09-705-398-20	Sequence 20, Appl
42	496.5	75.8	122	5	PCT-US93-07832-20	Sequence 20, Appl
43	495.5	75.6	122	2	US-07-934-373C-45	Sequence 45, Appl
44	495.5	75.6	122	3	US-08-437-642B-45	Sequence 45, Appl
45	495.5	75.6	122	4	US-08-146-206C-26	Sequence 26, Appl

ALIGNMENTS

```
RESULT 1
US-09-440-781-96
Sequence 96, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-Yee Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 96
LENGTH: 118
TYPE: PRT
ORGANISM: artificial sequence
FEATURES:
NAME/KEY: artificial
LOCATION: 1-118
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-96

Query Match      100.0%; Score 655; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.2e-59;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 EVOLVESGGGLVOPGSLRLSCAASGTFSTYYGMMWVROAPGKLEWGWINTYGEPT 60
Db 1 EVOLVESGGGLVOPGSLRLSCAASGTFSTYYGMMWVROAPGKLEWGWINTYGEPT 60
Cy 61 AADPKRFTFSLDPSKSTAYLQNNSLRAEDTAVYYCAKPHYGSSHHWYFDVWGQCTL 118
Db 61 AADPKRFTFSLDPSKSTAYLQNNSLRAEDTAVYYCAKPHYGSSHHWYFDVWGQCTL 118

RESULT 2
US-09-440-781-97
Sequence 97, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-Yee Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 97
LENGTH: 118
TYPE: PRT
ORGANISM: artificial sequence
FEATURES:
```

NAME/KEY: artificial
LOCATION: 1-118
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-97

Query Match 98.3%; Score 644; DB 4; Length 118;
Best Local Similarity 98.3%; Pred. No. 4.2e-58;
Matches 116; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKGLVWGIMINTYGEPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKGLVWGIMINTYGEPT 60

QY 61 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 118
DB 61 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 118

RESULT 3
US-09-440-781-98
Sequence 98, Application US/09440781
Patent No. 6632926

GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99

SEQ ID NO 98
LENGTH: 121
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-121
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-98

Query Match 96.4%; Score 631.5; DB 4; Length 121;
Best Local Similarity 95.9%; Pred. No. 8e-57;
Matches 116; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKGLVWGIMINTYGEPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKGLVWGIMINTYGEPT 60

QY 61 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHY--GSSHWYFDVWGQGT 117
DB 61 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYVNERKSHWYFDVWGQGT 120

QY 118 L 118
DB 121 L 121

RESULT 4
US-10-011-125A-2
Sequence 2, Application US/10011125A
Patent No. 6828121

GENERAL INFORMATION:
APPLICANT: Chen, Christina Yu-Ching
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1804R1
CURRENT APPLICATION NUMBER: US/10/011,125A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 12

SEQ ID NO 2
LENGTH: 491
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Sequence is synthesized.
Patent No. 6828121
US-10-011-125A-2

Query Match 96.3%; Score 631; DB 4; Length 491;
Best Local Similarity 94.2%; Pred. No. 4.7e-56;
Matches 112; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKGLVWGIMINTYGEPT 60
DB 261 EVOLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKGLVWGIMINTYGEPT 320

QY 61 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 118
DB 321 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 378

RESULT 5
US-09-440-781-99
Sequence 99, Application US/09440781
Patent No. 6632926

GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99

SEQ ID NO 99
LENGTH: 121
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-121
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-99

Query Match 94.7%; Score 620.5; DB 4; Length 121;
Best Local Similarity 94.2%; Pred. No. 1e-55;
Matches 114; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKGLVWGIMINTYGEPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKGLVWGIMINTYGEPT 60

QY 61 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHY--GSSHWYFDVWGQGT 117
DB 61 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYVNERKSHWYFDVWGQGT 120

QY 118 L 118
DB 121 L 121

RESULT 6
US-08-425-336-126
Sequence 126, Application US/08425336
Patent No. 5621083

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studilka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA

SEQUENCE: 11111018

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
TELEPHONE: 312/474-0448
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-425-336-126

Query Match 78.4%; Score 513.5; DB 1; Length 118;
Best Local Similarity 78.6%; Pred. No. 7.5e-45;
Matches 92; Conservative 12; Mismatches 8; Indels 5; Gaps 1;
Qy 1 EVLVSSGGGLVOPGSLRLSCAASGYFTFTNYGMNWRQAPGKGLRWGINTYGEPTY 60
Db 1 EIQLVSSGGGLVOPGSLRLSCAASGYFTFTNYGMNWRQAPGKGLRWGINTYGEPTY 60
Qy 61 AADFRRTFSLDPSKNTAVYQINSLRADTAIVYCAKPHYSSHWYFDWGGGT 117
Db 61 ADFRGRFTSLDPSKNTAVYQINSLRADTAIVYCAKPHYSSHWYFDWGGGT 112

RESULT 7
US-08-488-113B-126
Sequence 126, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B

FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-126

Query Match 78.4%; Score 513.5; DB 1; Length 118;
Best Local Similarity 78.6%; Pred. No. 7.5e-45;
Matches 92; Conservative 12; Mismatches 8; Indels 5; Gaps 1;
Qy 1 EVLVSSGGGLVOPGSLRLSCAASGYFTFTNYGMNWRQAPGKGLRWGINTYGEPTY 60
Db 1 EIQLVSSGGGLVOPGSLRLSCAASGYFTFTNYGMNWRQAPGKGLRWGINTYGEPTY 60
Qy 61 AADFRRTFSLDPSKNTAVYQINSLRADTAIVYCAKPHYSSHWYFDWGGGT 117
Db 61 ADFRGRFTSLDPSKNTAVYQINSLRADTAIVYCAKPHYSSHWYFDWGGGT 112

RESULT 8
US-08-477-484B-126
Sequence 126, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-646-360-126

Query Match 78.4%; Score 513.5; DB 2; Length 118;
Best Local Similarity 78.6%; Pred. No. 7.Se-45;
Matches 92; Conservative 12; Mismatches 8; Indels 5; Gaps 1;

Qy 1 EVLVESGGGLVOPGGSLRLSCAASGTFITNYGMNVRQAPGKLEWGVGINTYTGPTY 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 EQLVOSGGGLVKPGGSVRISCAASGYFTNYGMNVRQAPGKLEWGMGINTHTGPTY 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 AADFKERFTFLDTSKSTAYLQNSLRABETAIVYCAKYPHYGSSHWYFDVWGQGT 117
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 ADSEFKGRFTFLDSDSKNTAYLQINSRAEDTAVYFCTRRGY-----DWYFDVWGQGT 112
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RESULT 10
US-08-839-765-126
; Sequence 126, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-839-765-126

Query Match 78.4%; Score 513.5; DB 3; Length 118;
Best Local Similarity 78.6%; Pred. No. 7.5e-45;
Matches 92; Conservative 12; Mismatches 8; Indels 5; Gaps 1;
QY 1 EVOLVSGGLVPGGSLRLSCAASGYFTNYGMNVRQAPGKLEWGVNTHYTGEPT 60
Db 1 EQLVSGGLVPGGSLRLSCAASGYFTNYGMNVRQAPGKLEWGVNTHYTGEPT 60
QY 61 AADFKRFTSLDTSKSTAYLQNSLRADTAVYCAKYPHYGSSHWYFDVWGQGT 117
Db 61 ADSFKGRFTSLDTSKSTAYLQNSLRADTAVYCAKYPHYGSSHWYFDVWGQGT 112

RESULT 11
US-09-136-389-126
Sequence 126, Application US/09136389
Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360

FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-126
Query Match 78.4%; Score 513.5; DB 3; Length 118;
Best Local Similarity 78.6%; Pred. No. 7.5e-45;
Matches 92; Conservative 12; Mismatches 8; Indels 5; Gaps 1;
QY 1 EVOLVSGGLVPGGSLRLSCAASGYFTNYGMNVRQAPGKLEWGVNTHYTGEPT 60
Db 1 EQLVSGGLVPGGSLRLSCAASGYFTNYGMNVRQAPGKLEWGVNTHYTGEPT 60
QY 61 AADFKRFTSLDTSKSTAYLQNSLRADTAVYCAKYPHYGSSHWYFDVWGQGT 117
Db 61 ADSFKGRFTSLDTSKSTAYLQNSLRADTAVYCAKYPHYGSSHWYFDVWGQGT 112
RESULT 12
US-09-610-838-126
Sequence 126, Application US/09610838
Patent No. 6376217
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:


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; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-113B-147

Query Match 78.4%; Score 513.5; DB 1; Length 240;
Best Local Similarity 78.6%; Pred. No. 1.7e-44;
Matches 92; Conservative 12; Mismatches 8; Indels 5; Gaps 1;

Qy 1 EVLVESGGGLVOPGGSLRLSCAASGYTFTNYGMNVRQAPGKGLWVGWINTYTGEPTY 60
Db 123 EIQLVQSGGGLVPGGSLRLSCAASGYTFTNYGMNVRQAPGKGLWVGWINTYTGEPTY 182
Qy 61 AADPKRFTSLDTSKSTAYLQNSLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 117
Db 183 ADSFKGRFTSLDSDSKNTAYLQINSLRADTAIVYFCTRRGY-----DWFYFDVWGQGT 234

RESULT 15
US-08-488-113B-148
; Sequence 148, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-113B-148

Query Match 78.4%; Score 513.5; DB 1; Length 240;
Best Local Similarity 78.6%; Pred. No. 1.7e-44;
Matches 92; Conservative 12; Mismatches 8; Indels 5; Gaps 1;

Qy 1 EVLVESGGGLVOPGGSLRLSCAASGYTFTNYGMNVRQAPGKGLWVGWINTYTGEPTY 60
Db 1 EIQLVQSGGGLVPGGSLRLSCAASGYTFTNYGMNVRQAPGKGLWVGWINTYTGEPTY 60
Qy 61 AADPKRFTSLDTSKSTAYLQNSLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 117
Db 61 ADSFKGRFTSLDSDSKNTAYLQINSLRADTAIVYFCTRRGY-----DWFYFDVWGQGT 112

Search completed: March 14, 2005, 20:43:51
Job time : 25.3246 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 14, 2005, 20:21:17 ; Search time 94.4518 Seconds
(without alignments)
483.186 Million cell updates/sec

Title: US-09-723-752B-7
Perfect score: 655
Sequence: 1 EVQLVDSGGGLVQPGGSLRL.....YPHYGSHWFDVWGQSTL 118

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : A_Geneseq_16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003s.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	100.0	118	2	Aaw70678
2	655	100.0	118	3	Aab05899 Humanised
3	655	100.0	118	3	Aab13381 F(ab)-12
4	655	100.0	118	3	Aab13389 Anti-VEGF
5	655	100.0	118	5	Abp61247 Humanised
6	655	100.0	123	2	Aaw70617
7	655	100.0	123	5	Abp61186 Humanised
8	655	100.0	123	8	Adg31767 V(H) doma
9	655	100.0	123	8	Adg31780 V(H) doma
10	655	100.0	231	7	Adc26155 Parent an
11	655	100.0	476	8	Adg90736 Anti-VEGF
12	651	99.4	118	2	Aaw70680
13	651	99.4	118	5	Abp61249 Humanised
14	650	99.2	123	8	Adg31892 V(H) prot
15	649	99.1	123	8	Adg31895 V(H) prot
16	644	98.3	118	2	Aaw70682
17	644	98.3	118	3	Aab05900
18	644	98.3	118	3	Aab13382
19	644	98.3	118	5	Abp61251 Humanised
20	644	98.3	123	8	Adg31894 V(H) prot
21	644	98.3	231	7	Adc26158 Anti-VEGF
22	642	98.0	118	2	Aaw70684
23	642	98.0	118	3	Aab13383
24	642	98.0	118	5	Abp61253 Humanised
25	638	97.4	123	2	Aaw70626 Humanised

ALIGNMENTS

RESULT 1

AAW70678
ID AAW70678 standard; peptide; 118 AA.

AC AAW70678;

DT 27-JAN-1999 (first entry)

DE Anti-VEGF humanised antibody variable heavy domain of variant Y0101.

XX Heavy variable domain; murine; humanised antibody;

KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;

KW VEGF-induced angiogenesis; tumour; retinal disorder;

KW age-related macular degeneration; diabetic retinopathy;

KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

XX Synthetic.

OS Mus sp.

OS Homo sapiens.

PN WO9845331-A2.

XX 15-OCT-1998.

PD 03-APR-1998; 98WO-US006604.

XX 07-APR-1997; 97US-00833504.

PR 06-AUG-1997; 97US-00908469.

XX (GETH) GENENTECH INC.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI; 1998-568337/48.

XX New humanised antibody with affinity for vascular endothelial growth factor - for treatment of tumours, retinal disease and other angiogenic states, also related nucleic acid, vectors and transformed cells.

XX Example 3; Fig 9B; 100pp; English.

XX The present sequence represents a variable heavy domain of an affinity-matured anti-vascular endothelial growth factor (anti-VEGF) antibody variant. The sequence is used in the course of the invention to produce the humanised anti-VEGF antibody of the invention. The humanised antibodies are used to inhibit VEGF-induced angiogenesis, particularly for treating or preventing tumours (of any type) and retinal disorders (e.g. age-related macular degeneration or diabetic retinopathy). They can

Abp61195 Humanised
Adg31896 V(H) prot
Adc26162 Anti-VEGF
Aaw70676 Anti-VEGF
Abp61245 Humanised
Adg31897 V(H) prot
Aaw70686 Anti-VEGF
Aaw70688 Anti-VEGF
Aab13385 Anti-VEGF
Aab13384 Anti-VEGF
Abp61255 Humanised
Abp61257 Humanised
Adg31769 V(H) doma
Abp51953 Plasmid p
Abb81110 Anti-VEGF
Ado14129 Plasmid p
Adg90730 Anti-VEGF
Aaw86808 Variable
Aab05901 F(ab)-12
Aab13390 Anti-VEGF

26 638 97.4 123 5 ABP61195
27 638 97.4 123 8 ADG31896
28 638 97.4 231 7 ADC26162
29 637 97.3 118 2 AAW70676
30 637 97.3 118 5 ABP61245
31 636 97.1 123 8 ADG31897
32 635 96.9 118 2 AAW70686
33 635 96.9 118 2 AAW70688
34 635 96.9 118 3 AAB13385
35 635 96.9 118 3 AAB13384
36 635 96.9 118 5 ABP61255
37 635 96.9 118 5 ABP61257
38 635 96.9 123 8 ADG31769
39 635 96.9 254 5 ABP51953
40 635 96.9 476 5 ABB81110
41 635 96.9 476 8 ADO14129
42 635 96.9 476 8 ADG90730
43 634 96.8 123 2 AAW86808
44 631.5 96.4 121 3 AAB05901
45 631.5 96.4 121 3 AAB13390

CC also be used to treat other conditions that involve angiogenesis, e.g.
 CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
 XX
 SQ Sequence 118 AA;

Query Match 100.0%; Score 655; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 4.5e-55;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNWVRQAPGKGLVWGWINTYTGPTY 60
 |||||
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNWVRQAPGKGLVWGWINTYTGPTY 60
 |||||

QY 61 AADFKRRFTSLDTSKSTAYLQMSLAEDTAVYCAKYPHYGSSHWYFDVWGQGTLL 118
 |||||
 DB 61 AADFKRRFTSLDTSKSTAYLQMSLAEDTAVYCAKYPHYGSSHWYFDVWGQGTLL 118
 |||||

RESULT 2
 AAB05899
 ID AAB05899 standard; peptide; 118 AA.
 XX
 AC AAB05899;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Humanised anti-VEGF antibody F(ab)-12 heavy chain variable domain.
 XX
 KW Humanised; F(ab)-12; heavy chain variable domain; antibody variant;
 KW phage display; randomised library; cytostatic; antiarthritic;
 KW antiporiatic; antidiabetic; antiinflammatory; antiarteriosclerotic;
 KW vascular endothelial growth factor; VEGF; breast cancer; lung cancer;
 KW retinoblastoma; rheumatoid arthritis; psoriasis; atherosclerosis;
 KW diabetic retinopathy; complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200029584-A1.
 XX
 PD 25-MAY-2000.
 XX
 PF 16-NOV-1999; 99WO-US027153.
 XX
 PR 18-NOV-1998; 98US-0108945P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Chen YM, Lowman HB, Muller Y;
 XX
 DR WPI; 2000-387797/33.
 XX
 PT Antibody variants with higher binding affinity than native antibodies
 PT useful for diagnosis, prevention and treatment of neoplastic and non-
 PT neoplastic diseases comprises amino acid insertion in hypervariable
 FT region.
 XX
 PS Disclosure; Fig 1B; 110pp; English.
 XX
 CC The present sequence is the heavy chain variable domain of F(ab)-12, a
 CC humanised anti-vascular endothelial growth factor (VEGF) antibody. F(ab)-
 CC 12 was the parent antibody used in the production of a large number of
 CC antibody variants containing randomised peptide inserts within the
 CC complementarity determining regions (CDRs). Phage display libraries were
 CC subjected to eight rounds of selection to isolate variants with an
 CC antigen binding affinity at least two-fold stronger than the binding
 CC affinity of parent antibody for the target VEGF antibody. The anti-VEGF
 CC antibody variants may be useful in diagnostic assays for detecting
 CC the expression of VEGF in cells, tissue or serum. They may also be used in
 CC the prevention and treatment of neoplastic diseases such as breast
 CC cancer, lung cancer and retinoblastoma, and non-neoplastic diseases
 CC including rheumatoid arthritis, psoriasis, atherosclerosis, and diabetic
 CC and other proliferative retinopathies

XX SQ Sequence 118 AA;

Query Match 100.0%; Score 655; DB 3; Length 118;
 Best Local Similarity 100.0%; Pred. No. 4.5e-55;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNWVRQAPGKGLVWGWINTYTGPTY 60
 |||||
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNWVRQAPGKGLVWGWINTYTGPTY 60
 |||||

QY 61 AADFKRRFTSLDTSKSTAYLQMSLAEDTAVYCAKYPHYGSSHWYFDVWGQGTLL 118
 |||||
 DB 61 AADFKRRFTSLDTSKSTAYLQMSLAEDTAVYCAKYPHYGSSHWYFDVWGQGTLL 118
 |||||

RESULT 3
 AAB13381
 ID AAB13381 standard; protein; 118 AA.
 XX
 AC AAB13381;
 XX
 DT 12-SEP-2003 (revised)
 DT 21-NOV-2000 (first entry)
 XX
 DE F(ab)-12 anti-VEGF antibody heavy chain variable domain.
 XX
 KW Humanised; F(ab)-12; vascular endothelial cell growth factor; VEGF;
 KW antibody; antiinflammatory; cerebroprotective; cytostatic; antirheumatic;
 KW antiarthritic; antiporiatic; antiarteriosclerotic; antidiabetic;
 KW antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
 KW psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
 KW neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
 KW tissue transplantation; inflammation; oedema; trauma;
 KW complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 PH Key Location/Qualifiers
 FT Region 26..35 /label= CDR-H1
 FT Region 50..66 /label= CDR-H2
 FT Region 70..79 /label= CDR-7
 FT Region 99..112 /label= CDR-H3
 XX
 PN WO200037502-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 09-DEC-1999; 99WO-US029475.
 XX
 PR 22-DEC-1998; 98US-00218481.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Van Bruggen N, Ferrara N;
 XX
 DR WPI; 2000-442646/38.
 XX
 PT Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,
 PT diabetes and chronic inflammation in a mammal, comprises administering a
 PT human vascular endothelial cell growth factor antagonist.
 XX
 PS Disclosure; Fig 14B; 60pp; English.
 XX
 CC The present sequence is the heavy chain variable domain of humanised anti-
 CC -vascular endothelial cell growth factor (anti-VEGF) antibody F(ab)-12.
 CC It may be used to treat conditions characterised by undesirable excessive

CC neovascularisation. Such conditions include tumours (especially solid
 CC ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
 CC other retinopathies, retrolental fibroplasia, age-related macular
 CC degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias
 CC (including Grave's disease), corneal and other tissue transplantation,
 CC and chronic inflammation. Oedemas associated with tumours, strokes and
 CC head trauma, and ascites associated with malignancies, meigs syndrome,
 CC lung inflammation, nephrotic syndrome, pericardial effusion and pleural
 CC effusion, may also be treated. Affinity matured anti-VEGF antibodies are
 CC also used as therapeutic agents. Monoclonal antibodies are generated in
 CC hybridoma cells and those with affinity for VEGF are identified by
 CC immunoprecipitation or by an in vitro binding assay. (Updated on 12-SEP-
 CC 2003 to standardise OS field)

XX Sequence 118 AA;

Query Match 100.0%; Score 655; DB 3; Length 118;
 Best Local Similarity 100.0%; Pred. No. 4.5e-55;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNYGMNWRQAPGKGLVWGWINTYTGPTY 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNYGMNWRQAPGKGLVWGWINTYTGPTY 60

Qy 61 AADPKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGL 118
 Db 61 AADPKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGL 118

RESULT 4

AA13389 ID AA13389 standard; protein; 118 AA.

XX AC AA13389;

XX DT 21-NOV-2000 (first entry)

XX Anti-VEGF antibody Y0192 heavy chain variable domain.

XX Y0192; vascular endothelial cell growth factor; VEGF; antibody;
 KW antiinflammatory; cerebroprotective; cytostatic; antirheumatic;
 KW antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic;
 KW antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
 KW psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
 KW neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
 KW tissue transplantation; inflammation; oedema; trauma;
 KW complementarity determining region; CDR.

XX Unidentified.

Key	Region	Location/Qualifiers
FT	Region	26...35 /label= CDR-H1
FT	Region	50...66 /label= CDR-H2
FT	Region	70...79 /label= CDR-7
FT	Region	99...112 /label= CDR-H3

XX WO200037502-A2.

XX 29-JUN-2000.

XX 09-DEC-1999; 99WO-US029475.

XX 22-DEC-1998; 98US-00218481.

XX (GETH) GENENTECH INC.

XX Van Bruggen N, Ferrara N;

XX WPI; 2000-442646/38.

XX

PT Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,
 PT diabetes and chronic inflammation in a mammal, comprises administering a
 PT human vascular endothelial cell growth factor antagonist.

PS Disclosure; Fig 15B; 60pp; English.

XX The present sequence is the heavy chain variable region of the affinity
 CC matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody
 CC Y0192. Humanised F(ab)-12 and affinity matured anti-VEGF antibodies may
 CC be used to treat conditions characterised by undesirable excessive
 CC neovascularisation. Such conditions include tumours (especially solid
 CC ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
 CC other retinopathies, retrolental fibroplasia, age-related macular
 CC degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias
 CC (including Grave's disease), corneal and other tissue transplantation,
 CC and chronic inflammation. Oedemas associated with tumours, strokes and
 CC head trauma, and ascites associated with malignancies, meigs syndrome,
 CC lung inflammation, nephrotic syndrome, pericardial effusion and pleural
 CC effusion, may also be treated. Monoclonal antibodies are generated in
 CC hybridoma cells and those with affinity for VEGF are identified by
 CC immunoprecipitation or by an in vitro binding assay

XX Sequence 118 AA;

Query Match 100.0%; Score 655; DB 3; Length 118;
 Best Local Similarity 100.0%; Pred. No. 4.5e-55;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNYGMNWRQAPGKGLVWGWINTYTGPTY 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNYGMNWRQAPGKGLVWGWINTYTGPTY 60

Qy 61 AADPKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGL 118

Db 61 AADPKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGL 118

RESULT 5

ABP61247 ID ABP61247 standard; protein; 118 AA.

XX AC ABP61247;

XX DT 20-SEP-2002 (first entry)

XX Humanised anti-VEGF Y0101 antibody variable heavy domain.

XX Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
 KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
 KW retinal disorder; intraocular neovascular disorder; Y0101; heavy chain;
 KW variable domain.

XX Homo sapiens.

XX Mus sp.

XX Synthetic.

Key	Region	Location/Qualifiers
FT	Domain	26...35 /label= CDR-H1
FT	Domain	50...66 /label= CDR-H2
FT	Domain	70...79 /label= CDR-7
FT	Domain	99...112 /label= CDR-H3

XX US2002032315-A1.

XX 14-MAR-2002.

XX 06-APR-1998; 98US-00056160.

XX

PT mammal, particularly for treating tumor or retinal disorders.

PS Claim 7; Fig 1; 47pp; English.

XX The present invention relates to humanised anti-VEGF (vascular
CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
CC particularly those having a tumour or a retinal disorder e.g. intraocular
CC neovascular disorders. The present sequence is an exemplary heavy chain
CC variable domain of the humanised anti-VEGF antibody of the invention

XX Sequence 123 AA;

Query Match 100.0%; Score 655; DB 5; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.8e-55;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFNYGMNVRQAPGKGLVWGVWINTYTGEPTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFNYGMNVRQAPGKGLVWGVWINTYTGEPTY 60
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRAEDTAVYCAKYPHYGSSHWYFDVWGQGL 118
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRAEDTAVYCAKYPHYGSSHWYFDVWGQGL 118

RESULT 8

ADG31767
ID ADG31767 standard; protein; 123 AA.

XX AC ADG31767;

DT 26-FEB-2004 (first entry)

XX V(H) domain of parental humanised murine anti-VEGF antibody SeqID1.

XX protein library; in silico; VEGF; vascular endothelial growth factor;
KW antibody; computational prediction; V(H) domain; mouse; murine.

XX Synthetic.

OS Mus sp.

XX WO2003099999-A2.

XX 04-DEC-2003.

XX 20-MAY-2003; 2003WO-US016037.

XX 20-MAY-2002; 2002US-00153159.

PR 20-MAY-2002; 2002US-00153176.

XX (ABMA-) ABMAXIS INC.

XX Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S;

PI WPI; 2004-035117/03.

XX Constructing antibody libraries for generating protein libraries with
PT improved biological function comprising selecting from tester protein
PT sequences two peptide segments having 15% sequence identity with the lead
PT sequence.

XX Disclosure; SEQ ID NO 1; 354pp; English.

XX This invention relates to a novel method for the generation and screening
CC of a protein library in silico. Specifically, it refers to a high-
CC throughput method optimised for the identification of anti-VEGF (vascular
CC endothelial growth factor) antibodies with improved binding affinities
CC for their target antigen (VEGF), using computational prediction. The
CC present invention describes selecting proteins with a desirable function
CC based on their structural similarity to the target structural or
CC functional motif of a lead protein of interest. Accordingly, these

CC protein libraries are functionally biased with increased diversity so as
CC to increase the chance of identifying novel hits or combinations of
CC mutants with enhanced binding affinity. Furthermore, the sequence profile
CC based on the multiple structure alignment of the available lead structure
CC allows the sampling of a larger sequence space than by traditional,
CC multiple sequence alignment approaches. This polypeptide sequence is the
CC V(H) domain of parental humanised murine anti-VEGF antibody, used in an
CC exemplification of the invention.

XX Sequence 123 AA;

Query Match 100.0%; Score 655; DB 8; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.8e-55;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFNYGMNVRQAPGKGLVWGVWINTYTGEPTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFNYGMNVRQAPGKGLVWGVWINTYTGEPTY 60
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRAEDTAVYCAKYPHYGSSHWYFDVWGQGL 118
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRAEDTAVYCAKYPHYGSSHWYFDVWGQGL 118

RESULT 9

ADG31780
ID ADG31780 standard; protein; 123 AA.

XX AC ADG31780;

DT 26-FEB-2004 (first entry)

XX V(H) domain of the anti-VEGF two chain antibody AM2 protein SeqID 14.

XX protein library; in silico; VEGF; vascular endothelial growth factor;
KW antibody; computational prediction; V(H) domain; flexon; AM2;
KW two chain antibody; murine; mouse.

XX Synthetic.

OS Unidentified.

OS Mus sp.

XX WO2003099999-A2.

XX 04-DEC-2003.

XX 20-MAY-2003; 2003WO-US016037.

XX 20-MAY-2002; 2002US-00153159.

PR 20-MAY-2002; 2002US-00153176.

XX (ABMA-) ABMAXIS INC.

XX Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S;

PI WPI; 2004-035117/03.

DR N-PSDB; ADG31779.

XX Constructing antibody libraries for generating protein libraries with
PT improved biological function comprising selecting from tester protein
PT sequences two peptide segments having 15% sequence identity with the lead
PT sequence.

XX Disclosure; SEQ ID NO 14; 354pp; English.

XX This invention relates to a novel method for the generation and screening
CC of a protein library in silico. Specifically, it refers to a high-
CC throughput method optimised for the identification of anti-VEGF (vascular
CC endothelial growth factor) antibodies with improved binding affinities
CC for their target antigen (VEGF), using computational prediction. The
CC present invention describes selecting proteins with a desirable function
CC based on their structural similarity to the target structural or
CC functional motif of a lead protein of interest. Accordingly, these

CC protein libraries are functionally biased with increased diversity so as
CC to increase the chance of identifying novel hits or combinations of
CC mutants with enhanced binding affinity. Furthermore, the sequence profile
CC based on the multiple structure alignment of the available lead structure
CC allows the sampling of a larger sequence space than by traditional,
CC multiple sequence alignment approaches. This polypeptide sequence is the
CC V(H) domain of the anti-VEGF two chain antibody AMU protein, used in an
CC exemplification of the invention.

XX Sequence 123 AA;

Qy Query Match 100.0%; Score 655; DB 8; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.8e-55;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNYGMNVRQAPGKGLVGVWINTYTGEPT 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNYGMNVRQAPGKGLVGVWINTYTGEPT 60
Qy 61 AADFKRRFTSLDTSKSTAYLQMNLSRAEDTAVYCAKYPHYGSSHWYFDVWGQGL 118
Db 61 AADFKRRFTSLDTSKSTAYLQMNLSRAEDTAVYCAKYPHYGSSHWYFDVWGQGL 118

RESULT 10

ID ADC26155 standard; protein; 231 AA.

XX ADC26155;

DT 18-DEC-2003 (first entry)

XX Parent anti-VEGF Y0101 antibody wild-type heavy chain protein.

XX antibody variant; cytostatic; cancer; parent; anti-VEGF;
KW vascular endothelial growth factor; Y0101; heavy chain; wild-type.
XX Unidentified.

PN WO2003068801-A2.

XX 21-AUG-2003.

PF 11-FEB-2003; 2003WO-US004184.

XX 11-FEB-2002; 2002US-035895P.

PR 10-SEP-2002; 2002US-0409685P.

XX (GETH) GENENTECH INC.

PI Lowman HB, Marvin JS;

XX WPI; 2003-697521/66.

XX Making an antibody variant of a parent antibody specific to an antigen by
PT identifying a target amino acid residue within the variable domain of the
PT parent antibody and substituting the target residue with a different
PT amino acid residue.

XX Example 1; SEQ ID NO 2; 81pp; English.

XX The invention relates to a novel method for making an antibody variant of
XX a parent antibody specific to an antigen. This is achieved via
CC identifying a target amino acid residue within the variable domain of the
CC parent antibody and substituting the target residue with a different
CC replacement amino acid residue such that the charge complementarity
CC between the antibody and antigen is increased. The antibody variant of
CC the invention demonstrates cytostatic activity whilst the method may be
CC useful for treating cancer. The current sequence is that of the parent
CC anti-VEGF (vascular endothelial growth factor) Y0101 antibody Fab
CC fragment heavy chain protein of the invention.

XX Sequence 231 AA;

Qy Query Match 100.0%; Score 655; DB 7; Length 231;
Best Local Similarity 100.0%; Pred. No. 9.6e-55;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNYGMNVRQAPGKGLVGVWINTYTGEPT 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNYGMNVRQAPGKGLVGVWINTYTGEPT 60

Qy 61 AADFKRRFTSLDTSKSTAYLQMNLSRAEDTAVYCAKYPHYGSSHWYFDVWGQGL 118

Db 61 AADFKRRFTSLDTSKSTAYLQMNLSRAEDTAVYCAKYPHYGSSHWYFDVWGQGL 118

RESULT 11

ADQ90736 standard; protein; 476 AA.

XX ADQ90736;

AC 21-OCT-2004 (first entry)

XX Anti-VEGF antibody heavy chain protein SEQ ID NO:19.

XX antibody; antigen binding fragment; cell culture; variable domain;
KW modified framework region; hypervariable region; cytostatic;
KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
KW tumour; inflammatory disorder; angiogenic disorder;
KW immunological disorder; anti-VEGF antibody;
KW anti vascular endothelial cell growth factor antibody; heavy chain.

XX Homo sapiens.

OS Synthetic.

XX WO2004065417-A2.

XX 05-AUG-2004.

XX 23-JAN-2004; 2004WO-US001844.

XX 23-JAN-2003; 2003US-0442484P.

XX (GETH) GENENTECH INC.

XX Simmons L;

XX WPI; 2004-562149/54.

XX N-PSDB; ADQ90720.

XX Producing an antibody or antigen binding fragment in high yield in a cell
PT culture, comprises expressing a variable domain with a modified framework
PT region in a host cell.

XX Example 6; SEQ ID NO 25; 161pp; English.

XX The present invention describes a method for producing an antibody or
CC antigen binding fragment in high yield in a cell culture. The method
CC comprises expressing a variable domain of the antibody or antigen binding
CC fragment comprising a modified framework region (FR) in a host cell, and
CC recovering the antibody or antigen binding fragment variable domain
CC comprising the modified framework from the host cell. The modified FR in
CC the method described above has a substitution of at least one amino acid
CC position with a different amino acid, where the different amino acid is
CC the amino acid found at the corresponding FR position of a human subgroup
CC variable domain consensus sequence that has a hypervariable region 1
CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
CC The antibody or antigen binding fragment variable domain comprises the
CC modified FR that has improved yield in cell culture compared to an
CC unmodified antibody or antigen-binding fragment. The antibody and antigen
CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
CC immunomodulatory activities, and can be used in antibody therapy. The
CC methods and compositions of the present invention are useful for

CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents the heavy chain of an anti-VEGF (vascular endothelial
 CC cell growth factor) antibody, which is used in the exemplification of the
 CC present invention.

XX Sequence 476 AA;
 SQ
 Query Match 100.0%; Score 655; DB 8; Length 476;
 Best Local Similarity 100.0%; Pred. No. 2.2e-54;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFNTYGMNWVRQAPCKGLEWVGWINTYTGEPY 60
 DB 24 EVQLVESGGGLVQPGGSLRLSCAASGYTFNTYGMNWVRQAPCKGLEWVGWINTYTGEPY 83
 QY 61 AADFKRRFTFSLDTSKSTAYLQMNLSRAEDTAVYCAKYPHYGSHWYFDVWGQGTLL 118
 DB 84 AADFKRRFTFSLDTSKSTAYLQMNLSRAEDTAVYCAKYPHYGSHWYFDVWGQGTLL 141

RESULT 12
 AAW70680
 ID AAW70680 standard; peptide; 118 AA.

XX AC AAW70680;
 XX DT 27-JAN-1999 (first entry)
 XX DE Anti-VEGF humanised antibody variable heavy domain of variant Y0192.
 XX KW Heavy variable domain; murine; humanised antibody;
 KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
 KW VEGF-induced angiogenesis; tumour; retinal disorder;
 KW age-related macular degeneration; diabetic retinopathy;
 KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

XX Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX WO9845331-A2.
 XX 15-OCT-1998.

XX 03-APR-1998; 98WO-US006604.
 XX 07-APR-1997; 97US-00833504.
 XX 06-AUG-1997; 97US-00908489.
 XX (GETH) GENENTECH INC.
 XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
 XX WPI; 1998-568337/48.
 XX New humanised antibody with affinity for vascular endothelial growth
 factor - for treatment of tumours, retinal disease and other angiogenic
 states, also related nucleic acid, vectors and transformed cells.
 XX Example 3; Fig 9B; 100pp; English.

XX The present sequence represents a variable heavy domain of an affinity-
 CC matured anti-vascular endothelial growth factor (anti-VEGF) antibody
 CC variant. The sequence is used in the course of the invention to produce
 CC the humanised anti-VEGF antibody of the invention. The humanised
 CC antibodies are used to inhibit VEGF-induced angiogenesis, particularly
 CC for treating or preventing tumours (of any type) and retinal disorders
 CC (e.g. age-related macular degeneration or diabetic retinopathy). They can
 CC also be used to treat other conditions that involve angiogenesis, e.g.

CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
 XX Sequence 118 AA;
 SQ

Query Match 99.4%; Score 651; DB 2; Length 118;
 Best Local Similarity 99.2%; Pred. No. 1.1e-54;
 Matches 117; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFNTYGMNWVRQAPCKGLEWVGWINTYTGEPY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFNTYGMNWVRQAPCKGLEWVGWINTYTGEPY 60
 QY 61 AADFKRRFTFSLDTSKSTAYLQMNLSRAEDTAVYCAKYPHYGSHWYFDVWGQGTLL 118
 DB 61 AADFKRRFTFSLDTSKSTAYLQMNLSRAEDTAVYCAKYPHYGSHWYFDVWGQGTLL 118

RESULT 13
 ABP61249
 ID ABP61249 standard; protein; 118 AA.

XX AC ABP61249;
 XX DT 20-SEP-2002 (first entry)
 XX DE Humanised anti-VEGF Y0192 antibody variable heavy domain.
 XX KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
 KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
 KW retinal disorder; intracocular neovascular disorder; Y0192; heavy chain;
 KW variable domain.

XX Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 XX Key Location/Qualifiers
 XX Domain 26..35 /label= CDR-H1
 XX Domain 50..66 /label= CDR-H2
 XX Domain 70..79 /label= CDR-7
 XX Domain 99..112 /label= CDR-H3

XX US2002032315-A1.

XX 14-MAR-2002.
 XX 06-APR-1998; 98US-00056160.
 XX 06-AUG-1997; 97US-0054856P.

XX (BACA/) BACA M.
 XX (WELL/) WELLS J A.
 XX (PREST/) PRESTA L G.
 XX (LOWM/) LOWMAN H B.
 XX (CHEN/) CHEN Y M.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
 XX WPI; 2002-517920/55.

XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies
 or their variants, useful for inhibiting VEGF-induced angiogenesis in a
 mammal, particularly for treating tumor or retinal disorders.

XX Example 3; Fig 9; 47pp; English.

XX The present invention relates to humanised anti-VEGF (vascular
 endothelial growth factor) antibodies or a variant of a parent anti-VEGF
 antibody, which binds human VEGF. The anti-VEGF antibodies are useful for

CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
CC particularly those having a tumour or a retinal disorder e.g. intraocular
CC neovascular disorders. The present sequence is an exemplary heavy chain
CC variable domain of the humanised anti-VEGF antibody of the invention
XX
SQ Sequence 118 AA;

Query Match 99.4%; Score 651; DB 5; Length 118;
Best Local Similarity 99.2%; Pred. No. 1.1e-54;
Matches 117; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNVRAQPGKGLVWGWIINTYGEPT 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNVRAQPGKGLVWGWIINTYGEPT 60
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPHYGSSHWYFDVWGQGTLL 118
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPHYGSSHWYFDVWGQGTLL 118

RESULT 14
ADG31892
ID ADG31892 standard; peptide; 123 AA.
XX
AC ADG31892;
XX
DT 26-FEB-2004 (first entry)
XX
DE V(H) protein sequence of anti-VEGF antibody X64 SeqID 126.
XX
KW protein library; in silico; VEGF; vascular endothelial growth factor;
KW antibody; computational prediction; V(H) domain.
XX
OS Unidentified.

XX WO2003099999-A2.
XX
XX 04-DEC-2003.
XX
XX 20-MAY-2003; 2003WO-US016037.
XX
XX 20-MAY-2002; 2002US-00153159.
XX
XX 20-MAY-2002; 2002US-00153176.
XX
XX (ABMA-) ABMAXIS INC.
XX
XX Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S;
XX WPI; 2004-035117/03.

XX Constructing antibody libraries for generating protein libraries with
XX improved biological function comprising selecting from tester protein
XX sequences two peptide segments having 15% sequence identity with the lead
XX sequence.

XX Disclosure; SEQ ID NO 126; 354pp; English.

XX This invention relates to a novel method for the generation and screening
XX of a protein library in silico. Specifically, it refers to a high-
XX throughput method optimised for the identification of anti-VEGF (vascular
XX endothelial growth factor) antibodies with improved binding affinities
XX for their target antigen (VEGF), using computational prediction. The
XX present invention describes selecting proteins with a desirable function
XX based on their structural similarity to the target structural or
XX functional motif of a lead protein of interest. Accordingly, these
XX protein libraries are functionally biased with increased diversity so as
XX to increase the chance of identifying novel hits or combinations of
XX mutants with enhanced binding affinity. Furthermore, the sequence profile
XX based on the multiple structure alignment of the available lead structure
XX allows the sampling of a larger sequence space than by traditional,
XX V(H) protein sequence alignment approaches. This polypeptide sequence is the
XX exemplification of the invention.

XX
SQ Sequence 123 AA;

Query Match 99.2%; Score 650; DB 8; Length 123;
Best Local Similarity 99.2%; Pred. No. 1.4e-54;
Matches 117; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNVRAQPGKGLVWGWIINTYGEPT 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNVRAQPGKGLVWGWIINTYGEPT 60
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPHYGSSHWYFDVWGQGTLL 118
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPHYGSSHWYFDVWGQGTLL 118

RESULT 15
ADG31895
ID ADG31895 standard; peptide; 123 AA.
XX
AC ADG31895;
XX
DT 26-FEB-2004 (first entry)
XX
DE V(H) protein sequence of anti-VEGF antibody D36 SeqID 129.
XX
KW protein library; in silico; VEGF; vascular endothelial growth factor;
KW antibody; computational prediction; V(H) domain.
XX
OS Unidentified.

XX WO2003099999-A2.
XX
XX 04-DEC-2003.
XX
XX 20-MAY-2003; 2003WO-US016037.
XX
XX 20-MAY-2002; 2002US-00153159.
XX
XX 20-MAY-2002; 2002US-00153176.

XX (ABMA-) ABMAXIS INC.
XX
XX Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S;
XX WPI; 2004-035117/03.

XX Constructing antibody libraries for generating protein libraries with
XX improved biological function comprising selecting from tester protein
XX sequences two peptide segments having 15% sequence identity with the lead
XX sequence.

XX Disclosure; SEQ ID NO 129; 354pp; English.

XX This invention relates to a novel method for the generation and screening
XX of a protein library in silico. Specifically, it refers to a high-
XX throughput method optimised for the identification of anti-VEGF (vascular
XX endothelial growth factor) antibodies with improved binding affinities
XX for their target antigen (VEGF), using computational prediction. The
XX present invention describes selecting proteins with a desirable function
XX based on their structural similarity to the target structural or
XX functional motif of a lead protein of interest. Accordingly, these
XX protein libraries are functionally biased with increased diversity so as
XX to increase the chance of identifying novel hits or combinations of
XX mutants with enhanced binding affinity. Furthermore, the sequence profile
XX based on the multiple structure alignment of the available lead structure
XX allows the sampling of a larger sequence space than by traditional,
XX V(H) protein sequence alignment approaches. This polypeptide sequence is the
XX exemplification of the invention.

XX
SQ Sequence 123 AA;

Query Match 99.1%; Score 649; DB 8; Length 123;

Best Local Similarity 98.3%; Pred. No. 1.8e-54;
 Matches 116; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY	1	EVQLVESGGGLVQPGGSLRLS	CAASGYTF	TNYGMNVRQAPGK	GLEWVGWINTY	TGPTY	60
Db	1	EVQLVQSGGGVQPGGSLRLS	CAASGYTF	TNYGMNVRQAPGK	GLEWVGWINTY	TGPTY	60
QY	61	AADEFKRRPTFSLDTSKSTAY	LQNSLR	AEADTAVY	CAKYPHYGSSHWY	FDVWGQ	118
Db	61	AADEFKRRPTFSLDTSKSTAY	LQNSLR	AEADTAVY	CAKYPHYGSSHWY	FDVWGQ	118

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